

Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu  
 345 350 355  
 cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat 1219  
 Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp  
 360 365 370  
 ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag 1267  
 Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
 375 380 385  
 ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg 1315  
 Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
 390 395 400 405  
 gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt 1363  
 Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
 410 415 420  
 gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac 1411  
 Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
 425 430 435  
 gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct 1459  
 Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
 440 445 450  
 gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc 1507  
 Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
 455 460 465  
 ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat 1555  
 Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
 470 475 480 485  
 cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg 1603  
 Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
 490 495 500  
 gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac 1649  
 Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
 505 510  
 gatgcgctgt gtg 1662

&lt;210&gt; 348

&lt;211&gt; 513

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
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 Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser  
 20 25 30  
 Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
 35 40 45

Val Ala Gly Tyr Val Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
 355 360 365  
 Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg

370				375				380							
Leu 385	Tyr	Ser	Glu	Glu	Phe 390	Tyr	Thr	Leu	Ala	Arg 395	Ala	Arg	Leu	Asn	Glu 400
Gln	Gly	Arg	Met	Val 405	Val	Gln	Ser	Ser	Ser 410	Ala	Tyr	Thr	Thr	Pro 415	Asp
Val	Phe	Trp	Arg 420	Val	Gly	Ala	Thr	Leu 425	Lys	Ser	Ala	Gly	Cys 430	Glu	Gln
Val	Ile	Pro 435	Tyr	His	Val	His	Val 440	Pro	Thr	Phe	Gly	Asp 445	Trp	Gly	Phe
Gln	Leu 450	Cys	Gly	Pro	Ala	Asp 455	Met	Glu	Leu	Glu	Leu 460	Arg	Glu	Asp	Thr
Pro 465	Pro	Leu	Thr	Phe	Leu 470	Asn	Asp	Glu	Val	Leu 475	Val	Ala	Ala	Gly	Val 480
Phe	Gly	Leu	Asp	Asn 485	Gln	Pro	Arg	Glu	Leu 490	Glu	Pro	Ser	Thr	Leu 495	Asp
His	Pro	Arg	Val 500	Val	Glu	Asp	Leu	Arg 505	Lys	Gly	Tyr	Arg	Glu 510	Ser	Gly

Asp

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<210> 349
<211> 924
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(901)  
<223> RXA01757
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Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly Thr Phe Pro Gln Ala			
70	75	80	85
atc gag ggt gat gcg ctt ttt gag acg ctt gtc gac gcc ccg agc cgc			403
Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val Asp Ala Pro Ser Arg			
90	95		100
ctg cgg ggt aac ccc ata gac gct gct tca ggc agg ttc caa gca ggg			451
Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly Arg Phe Gln Ala Gly			
105	110		115
gcc tcc tcg ctt gcg ctc ggg ctt gca gcc cag ctc aag cca gga gtt			499
Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln Leu Lys Pro Gly Val			
120	125		130
tta gaa ctc ggg gac ccc gtc cat tct ctc agt gag gaa gat ggg gaa			547
Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser Glu Glu Asp Gly Glu			
135	140		145
atc gtt gtg aag tct tcc aaa cag att gtg agg gca aag cac gtc atc			595
Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg Ala Lys His Val Ile			
150	155		160
att gcg gtt cca ccg gca ctc gct gcc gag ttg att ggt ttc acc cta			643
Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu Ile Gly Phe Thr Leu			
170	175		180
gat tta cca gct gac gtg cga aaa gca gcg cat cca caa cat ata gct			691
Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His Pro Gln His Ile Ala			
185	190		195
gtg atg aat tgg gca aag gag aaa tac acc tta ccc aca caa gcc gca			739
Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu Pro Thr Gln Ala Ala			
200	205		210
tcg gct ggg ggt ttt ggg cat gag ctg ttc caa caa cca ctc gga cat			787
Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln Gln Pro Leu Gly His			
215	220		225
ggg cga att cat tgg gca tca acg gaa gtt gcc act gag ttt ggt gga			835
Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala Thr Glu Phe Gly Gly			
230	235	240	245
cac ctt gaa ggc gca gtt cgt gca gga att cag gct gcg ctt caa aca			883
His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln Ala Ala Leu Gln Thr			
250	255		260
gga ttt aat cta aaa tct taaacctcgt attttccctg ata			924
Gly Phe Asn Leu Lys Ser			
265			

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350



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<220>  
<221> CDS  
<222> (101)..(613)  
<223> RXA02159
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actgctgggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca																115
Met Ser Leu Gly Ser																5
1																
acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc																163
Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg																20
10 15																
caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag																211
Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln																35
25 30																
gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag																259
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln																50
40 45																
gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc																307
Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg																65
55 60																
ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc																355
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Gly Pro Val Asp Ser Ile																85
70 75																
gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt																403
Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu																95 100
90																
gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg																451
Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu																110 115
105																
cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg																499
Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg																120 125 130
135																
gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt																547
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val																140 145
150																
ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta																595
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu																155 160 165
170																
ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct																636
Leu Ser Gly Arg Thr Thr																

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val  
1 5 10 15

Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln  
                   20                                  25                                  30  
 Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly  
                   35                                  40                                  45  
 Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly  
                   50                                  55                                  60  
 Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly  
                   65                                  70                                  75                                  80  
 Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys  
                                   85                                  90                                  95  
 Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly  
                   100                                  105                                  110  
 Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala  
                   115                                  120                                  125  
 Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala  
                   130                                  135                                  140  
 Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys  
                   145                                  150                                  155                                  160  
 Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr  
                                   165                                  170

&lt;210&gt; 353

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(391)

&lt;223&gt; RXN02154

&lt;400&gt; 353

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caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115  
   Leu Lys Glu Gly Val  
   1  5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
                                   10                                  15                                  20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
                                   25                                  30                                  35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
                   40                                  45                                  50

ccttaaagcg gcg 414

Pro

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163

Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser	Val	Pro	Ala	Tyr	Leu	
				10					15					20		
gtt	ctt	gca	gac	gga	cgt	acc	ttc	acc	gga	ttt	ggc	ttt	gga	gct	atc	211
Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe	Gly	Phe	Gly	Ala	Ile	
			25					30					35			
ggc	acc	acc	ctt	ggt	gag	gca	gtg	ttc	act	acc	gcc	atg	acc	ggt	tac	259
Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
			40				45					50				
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
			55				60					65				
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
			70			75				80					85	
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac	ctc	403
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
				90					95					100		
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
			105					110					115			
atg	gca	ggc	cag	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc	gca	499
Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
			120				125					130				
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggt	tcc	att	gca	gcg	ggc	atc	ttc	547
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
			135				140				145					
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
					155					160					165	
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
				170					175					180		
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
			185				190						195			
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
			200				205					210				
tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
			215				220				225					
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
			230			235				240					245	
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	

250										255					260					
gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931				
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln					
		265						270					275							
att	ctt	ggc	cgc	gca	ttc	ggc	atg	gag	acc	tac	aag	ctg	aag	ttc	ggc	979				
Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly					
		280					285					290								
cac	cgc	ggc	atc	aac	gtt	cca	gtg	aag	aac	cac	atc	acc	ggc	aag	atc	1027				
His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His	Ile	Thr	Gly	Lys	Ile					
		295				300					305									
gac	atc	acc	gcc	cag	aac	cac	ggc	ttc	gca	ctc	aag	ggt	gaa	gca	ggc	1075				
Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu	Lys	Gly	Glu	Ala	Gly					
310					315					320					325					
cag	gaa	ttc	gag	acc	gat	ttc	ggc	act	gca	att	gtc	acc	cac	acc	tgc	1123				
Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile	Val	Thr	His	Thr	Cys					
				330					335						340					
ctc	aac	gac	ggc	gtc	gtt	gaa	ggt	att	gcg	ctg	aag	tcc	gga	cgc	gca	1171				
Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu	Lys	Ser	Gly	Arg	Ala					
			345					350					355							
tac	tcc	gtt	cag	tac	cac	cca	gag	gcc	gct	gcc	ggc	cca	aat	gat	gca	1219				
Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala	Gly	Pro	Asn	Asp	Ala					
		360					365					370								
agc	ccc	ctg	ttt	gac	cag	ttt	gtt	gag	ctg	atg	gat	gca	gac	gct	cag	1267				
Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met	Asp	Ala	Asp	Ala	Gln					
		375				380					385									
aag	aaa	ggc	gca	taaataacat	gccaaagcgt	tca										1302				
Lys	Lys	Gly	Ala																	
		390																		

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val	Ser	Lys	Asp	Thr	Thr	Thr	Tyr	Gln	Gly	Val	Thr	Glu	Ile	Gly	Ser
1				5					10					15	

Val	Pro	Ala	Tyr	Leu	Val	Leu	Ala	Asp	Gly	Arg	Thr	Phe	Thr	Gly	Phe
		20						25					30		

Gly	Phe	Gly	Ala	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr
		35					40					45			

Ala	Met	Thr	Gly	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg
	50					55					60				

Gln	Ile	Val	Val	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn
65					70					75					80

Asp	Glu	Asp	Asn	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85								90				95				
Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	
100								105				110				
Ser	Leu	Gln	Gln	Glu	Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	
115								120				125				
Ile	Asp	Thr	Arg	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	
130								135				140				
Ala	Ala	Gly	Ile	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	
145								150				155				
Leu	Val	Glu	Ile	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	
				165								170				
Ser	Val	Glu	Val	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	
180								185				190				
Glu	Glu	Arg	His	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	
195								200				205				
Thr	Pro	Arg	Arg	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	
210								215				220				
Ala	Glu	Thr	Pro	Phe	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	
225								230				235				
Phe	Ile	Ser	Asn	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	
				245								250				
Asp	Ile	Val	Arg	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	
260								265				270				
Cys	Phe	Gly	Asn	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	
275								280				285				
Lys	Leu	Lys	Phe	Gly	His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His	
290								295				300				
Ile	Thr	Gly	Lys	Ile	Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu	
305								310				315				
Lys	Gly	Glu	Ala	Gly	Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile	
				325								330				
Val	Thr	His	Thr	Cys	Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Ile	Ala	Leu	
340								345				350				
Lys	Ser	Gly	Arg	Ala	Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala	
355								360				365				
Gly	Pro	Asn	Asp	Ala	Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met	
370								375				380				
Asp	Ala	Asp	Ala	Gln	Lys	Lys	Gly	Ala								
385				390												

&lt;210&gt; 357

<211> 924  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(901)  
 <223> RXS00905

<400> 357

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tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
                               Met Thr Gln Phe Glu
                               1                               5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
                               10                               15                               20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
                               25                               30                               35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
                               40                               45                               50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
                               55                               60                               65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
   70                               75                               80                               85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
                               90                               95                               100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
                               105                               110                               115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
                               120                               125                               130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
                               135                               140                               145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595
Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
   150                               155                               160                               165

ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
                               170                               175                               180

gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
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Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195

cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr  
 200 205 210

gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225

gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245

gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260

ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15

Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30

Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45

Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60

Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80

Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95

Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110

Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys

165										170					175				
Pro	Glu	Leu	Phe	Asp	Ala	Asp	Val	Ile	Leu	Ile	Ala	Asp	Ser	Gly	Asn				
			180					185					190						
Ala	Ser	Val	Gly	Thr	Pro	Thr	Leu	Thr	Thr	Thr	Leu	Arg	Gly	Gly	Gly				
		195					200					205							
Gln	Val	Thr	Val	Thr	Val	Asp	Thr	Leu	Glu	Gly	Ala	Val	His	Ser	Gly				
	210					215					220								
Gln	Asn	Gly	Gly	Ala	Ala	Pro	Asp	Ala	Val	Ala	Ala	Leu	Val	Arg	Val				
225					230					235					240				
Leu	Asp	Thr	Leu	Arg	Asp	Glu	His	Gly	Arg	Thr	Val	Ile	Asp	Gly	Cys				
				245					250					255					
Gln	His	His	Arg	Lys	Leu	Glu	Gly	Arg	Ala	Leu									
			260					265											

&lt;210&gt; 359

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(604)

&lt;223&gt; RXS00906

&lt;400&gt; 359

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gctgttgctg	ctctcgtg	cggttctggat	actttgcgcg	atg	aac	acg	gac	gca		115
				Met	Asn	Thr	Asp	Ala		
				1				5		

ccg	tta	tcg	acg	gct	gtc	aac	acc	acc	gca	aac	tgg	aag	ggc	gag	cct		163
Pro	Leu	Ser	Thr	Ala	Val	Asn	Thr	Thr	Ala	Asn	Trp	Lys	Gly	Glu	Pro		
			10						15					20			

tat	gat	cca	gag	act	ttc	cgc	agc	gat	gcc	ggc	atc	ctc	gac	ggt	gta		211
Tyr	Asp	Pro	Glu	Thr	Phe	Arg	Ser	Asp	Ala	Gly	Ile	Leu	Asp	Gly	Val		
			25					30					35				

gac	atc	atg	ggc	gac	ggc	gac	aac	cca	gca	agc	atg	ctg	tgg	tcc	agg		259
Asp	Ile	Met	Gly	Asp	Gly	Asp	Asn	Pro	Ala	Ser	Met	Leu	Trp	Ser	Arg		
		40					45					50					

cct	gca	atc	tcc	atc	acc	gga	ttc	act	tcc	acc	cca	gtg	gca	gaa	gca		307
Pro	Ala	Ile	Ser	Ile	Thr	Gly	Phe	Thr	Ser	Thr	Pro	Val	Ala	Glu	Ala		
		55				60					65						

ctc	aac	gca	gtg	ccc	gca	acg	gcg	tcc	gcc	aag	cta	aac	ctt	cgc	gtg		355
Leu	Asn	Ala	Val	Pro	Ala	Thr	Ala	Ser	Ala	Lys	Leu	Asn	Leu	Arg	Val		
	70				75				80					85			

cca	gca	ggc	ctg	gaa	gca	aac	gat	gtg	gcc	gag	aag	ctg	aag	cag	cac		403
Pro	Ala	Gly	Leu	Glu	Ala	Asn	Asp	Val	Ala	Glu	Lys	Leu	Lys	Gln	His		
			90					95						100			

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
 105 110 115  
  
 gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
 120 125 130  
  
 acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
 135 140 145  
  
 acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu  
 150 155 160 165  
  
 gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

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 <211> 168  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 360  
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 Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
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 Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
 35 40 45  
  
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60  
  
 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80  
  
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95  
  
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110  
  
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125  
  
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu  
 130 135 140  
  
 Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys  
 145 150 155 160  
  
 Thr Glu Leu Ile Glu Val Asn Pro  
 165

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(223)  
 <223> RXS00907

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 actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115  
 Leu Ala Leu Tyr Gly  
 1 5  
 gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163  
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp  
 10 15 20  
 ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211  
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu  
 25 30 35  
 aac tac acc aag tagacccaaa agcaggcggtt aac 246  
 Asn Tyr Thr Lys  
 40

<210> 362  
 <211> 41  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 362  
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 Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu  
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 Ala Leu Phe Leu Leu Asn Tyr Thr Lys  
 35 40

<210> 363  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> RXS02001

<400> 363  
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 gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115

																Met	Pro	Val	Ile	Asn
																1				5
agt	atc	gcc	agt	ttt	tcc	gac	gag	atg	acc	cgc	tgg	cgg	cgt	cac	ctg	163				
Ser	Ile	Ala	Ser	Phe	Ser	Asp	Glu	Met	Thr	Arg	Trp	Arg	Arg	His	Leu					
				10					15					20						
cat	caa	aac	ccc	gaa	atc	agc	ttt	gat	tgt	gtg	gaa	act	gcg	gcc	ttc	211				
His	Gln	Asn	Pro	Glu	Ile	Ser	Phe	Asp	Cys	Val	Glu	Thr	Ala	Ala	Phe					
			25					30					35							
gtg	gcc	gag	cag	ctg	cgc	agc	ttc	ggg	gtg	gat	gaa	att	cac	acc	ggc	259				
Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp	Glu	Ile	His	Thr	Gly					
		40					45					50								
atc	gcg	aaa	acc	ggc	atc	atc	gcc	ctg	att	cac	ggg	cgc	gag	gct	ggc	307				
Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His	Gly	Arg	Glu	Ala	Gly					
	55					60					65									
ccc	gtc	gtc	ggc	ctg	cgc	gcc	gat	atg	gac	gcg	ctg	ccg	ctg	acc	gag	355				
Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala	Leu	Pro	Leu	Thr	Glu					
	70				75					80					85					
att	acc	ggc	gtc	gac	tat	gcc	tcg	acc	acc	ccc	gga	aaa	atg	cac	gcc	403				
Ile	Thr	Gly	Val	Asp	Tyr	Ala	Ser	Thr	Thr	Pro	Gly	Lys	Met	His	Ala					
				90					95					100						
tgc	ggc	cac	gac	ggc	cac	acg	acc	atg	ctg	ctg	ggc	gcc	gcc	aaa	tat	451				
Cys	Gly	His	Asp	Gly	His	Thr	Thr	Met	Leu	Leu	Gly	Ala	Ala	Lys	Tyr					
			105					110					115							
ctg	gcc	gag	acg	cgc	aat	ttc	gca	ggc	acc	gtc	gcg	ctg	atc	ttc	cag	499				
Leu	Ala	Glu	Thr	Arg	Asn	Phe	Ala	Gly	Thr	Val	Ala	Leu	Ile	Phe	Gln					
		120					125					130								
cct	gcg	gaa	gaa	aac	ggc	ggc	ggc	gcg	ggc	gtt	atg	gtc	gat	gaa	ggc	547				
Pro	Ala	Glu	Glu	Asn	Gly	Gly	Gly	Ala	Gly	Val	Met	Val	Asp	Glu	Gly					
	135				140						145									
gtc	ctc	gac	cgc	ttt	gcc	atc	gcc	gaa	gtc	tac	gcc	ctg	cac	aac	cag	595				
Val	Leu	Asp	Arg	Phe	Ala	Ile	Ala	Glu	Val	Tyr	Ala	Leu	His	Asn	Gln					
	150				155					160					165					
ccc	ggc	ctg	ccg	ctt	ggc	cat	ttt	atg	acg	aca	gcc	ggc	ccg	atc	atg	643				
Pro	Gly	Leu	Pro	Leu	Gly	His	Phe	Met	Thr	Thr	Ala	Gly	Pro	Ile	Met					
				170					175					180						
gcc	gct	gtc	gac	acg	ttc	gac	atc	aac	att	acc	gga	cgc	ggc	ggc	cac	691				
Ala	Ala	Val	Asp	Thr	Phe	Asp	Ile	Asn	Ile	Thr	Gly	Arg	Gly	Gly	His					
			185				190						195							
ggc	gcc	aaa	ccg	cac	caa	acc	cgc	gac	ccc	atc	gtc	gca	gcc	gtc	gga	739				
Gly	Ala	Lys	Pro	His	Gln	Thr	Arg	Asp	Pro	Ile	Val	Ala	Ala	Val	Gly					
		200					205					210								
att	gtc	caa	gcg	ttt	caa	acg	ata	gtc	agc	cgg	aat	cac	aat	ccg	gtc	787				
Ile	Val	Gln	Ala	Phe	Gln	Thr	Ile	Val	Ser	Arg	Asn	His	Asn	Pro	Val					
	215				220						225									
gag	gac	ctt	gtc	gtg	tcg	gtc	acg	caa	atc	cac	acc	ggc	agc	gcc	gat	835				
Glu	Asp	Leu	Val	Val	Ser	Val	Thr	Gln	Ile	His	Thr	Gly	Ser	Ala	Asp					

230	235	240	245	
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc				883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe				
250		255	260	
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc				931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val				
265		270	275	
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac				979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn				
280		285	290	
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct				1027
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala				
295		300	305	
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg				1075
Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser				
310		315	320	325
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg				1123
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro				
330		335	340	
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac				1171
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn				
345		350	355	
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc				1219
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe				
360		365	370	
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg				1268
Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly				
375		380	385	
cgctcgaaga tgc				1281

&lt;210&gt; 364

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

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Trp	Arg	Arg	His	Leu	His	Gln	Asn	Pro	Glu	Ile	Ser	Phe	Asp	Cys	Val
			20					25					30		

Glu	Thr	Ala	Ala	Phe	Val	Ala	Glu	Gln	Leu	Arg	Ser	Phe	Gly	Val	Asp
		35					40					45			

Glu	Ile	His	Thr	Gly	Ile	Ala	Lys	Thr	Gly	Ile	Ile	Ala	Leu	Ile	His
	50					55					60				

Gly	Arg	Glu	Ala	Gly	Pro	Val	Val	Gly	Leu	Arg	Ala	Asp	Met	Asp	Ala
65					70					75					80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro  
 85 90 95  
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu  
 100 105 110  
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val  
 115 120 125  
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val  
 130 135 140  
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr  
 145 150 155 160  
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr  
 165 170 175  
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr  
 180 185 190  
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile  
 195 200 205  
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg  
 210 215 220  
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His  
 225 230 235 240  
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly  
 245 250 255  
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg  
 260 265 270  
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala  
 275 280 285  
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala  
 290 295 300  
 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val  
 305 310 315 320  
 Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe  
 325 330 335  
 Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser  
 340 345 350  
 Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro  
 355 360 365  
 Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu  
 370 375 380  
 Lys Gly  
 385

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXS02101

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agtttttagtg tcgctgcgca ggtactctac tatctaattcc atg agc cgc att tca 115
                                         Met Ser Arg Ile Ser
                                         1           5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
                        10                      15                      20

tat cag gat ttc cac gaa cat cct gag ctg tcc ggc ttc gaa tca gag 211
Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
                        25                      30                      35

acc gca gat cgc att cag aaa tac ctg gag cgt ttt gat tgt gag gtg 259
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
                        40                      45                      50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
                        55                      60                      65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
                        70                      75                      80                      85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg
                        90                      95                      100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
                        105                      110                      115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
                        120                      125                      130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
                        135                      140                      145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
                        150                      155                      160                      165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
                        170                      175                      180

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ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691  
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala  
 185 190 195

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 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly  
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787  
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile  
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835  
 Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp  
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ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac 883  
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn  
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acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931  
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn  
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gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979  
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg  
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ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac 1027  
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr  
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 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr  
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 Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
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 Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
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gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac 1363  
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1386

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Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
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Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
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Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
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Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met  
145 150 155 160

Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe  
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Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro  
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Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly  
195 200 205

Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr  
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Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu  
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Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser  
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<div style="display: flex; justify-content: space-between;"> <div>atg cca aag cgt tca</div> <div>115</div> </div> <div style="display: flex; justify-content: space-between;"> <div>Met Pro Lys Arg Ser</div> <div></div> </div> <div style="display: flex; justify-content: space-between;"> <div></div> <div>15</div> </div>																
gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc																163
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Glu Pro Glu Tyr Ile	Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly		
70	75	80	85
cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt			403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu			
	90	95	100
aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc			451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly			
	105	110	115
gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat			499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp			
	120	125	130
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg			547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala			
	135	140	145
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca			595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala			
	150	155	160
gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc			643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly			
	170	175	180
ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct			691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala			
	185	190	195
ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa			739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu			
	200	205	210
tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc			787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr			
	215	220	225
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg			835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu			
	230	235	240
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg			883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu			
	250	255	260
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc			931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile			
	265	270	275
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc			979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile			
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Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val			
	295	300	305

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Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
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Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
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Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
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Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
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Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
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Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
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Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
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Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys	
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Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met	
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Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val	
520 525 530	
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Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro	
535 540 545	

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Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala	Ala	Glu	Ser	Glu	Val	
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Ala	Pro	Gln	Thr	Glu	Arg	Glu	Lys	Val	Leu	Ile	Leu	Gly	Ser	Gly	Pro	
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aac	cgc	atc	ggc	cag	ggc	atc	gag	ttc	gac	tac	tcc	tgt	gtt	cac	gca	1891
Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp	Tyr	Ser	Cys	Val	His	Ala	
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gct	ctt	gag	ctc	tcc	cgc	gtc	ggc	tac	gaa	act	gtc	atg	gtc	aac	tgc	1939
Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu	Thr	Val	Met	Val	Asn	Cys	
		600					605					610				
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Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp	Thr	Ala	Asp	Arg	Leu	Tyr	
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ttc	gag	cca	ctg	acc	ttc	gaa	gac	gtc	atg	gag	gtc	tac	cac	gct	gag	2035
Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met	Glu	Val	Tyr	His	Ala	Glu	
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Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile	Val	Gln	Leu	Gly	Gly	Gln	
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act	cct	ctg	ggc	ttg	gca	gat	cgt	ttg	aag	aag	gct	ggc	gtc	cct	gtc	2131
Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys	Lys	Ala	Gly	Val	Pro	Val	
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att	ggt	acc	tcc	cca	gag	gca	atc	gac	atg	gct	gag	gac	cgt	ggc	gag	2179
Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met	Ala	Glu	Asp	Arg	Gly	Glu	
		680					685					690				
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Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu	Pro	Ala	Pro	Ala	Phe	Gly	
	695					700					705					
acc	gca	acc	tct	ttc	gaa	gag	gct	cgc	aca	gta	gcc	gat	gag	atc	agc	2275
Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr	Val	Ala	Asp	Glu	Ile	Ser	
710					715					720					725	
tac	cca	gtg	ctg	gtt	cgc	cct	tcc	tac	gtc	ttg	ggt	ggc	cgt	ggc	atg	2323
Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val	Leu	Gly	Gly	Arg	Gly	Met	
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gag	att	gtc	tac	gat	gag	gct	tcc	ctc	gag	gat	tac	atc	aac	cgc	gca	2371
Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu	Asp	Tyr	Ile	Asn	Arg	Ala	
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Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val	Asp	Arg	Phe	Leu	Asp	
		760					765					770				
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Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	Cys	Asp	Gly	Asp	Glu	Val	
	775					780					785					
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Tyr 790	Leu	Ala	Gly	Val	Met 795	Glu	His	Ile	Glu	Glu 800	Ala	Gly	Ile	His	Ser 805	
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atc Ile	gag Glu	aag Lys 825	gtc Val	cgc Arg	gaa Glu	gca Ala	acc Thr	aag Lys 830	aag Lys	ctg Leu	gct Ala	ctg Leu	ggc Gly 835	atc Ile	ggt Gly	2611
gta Val	cag Gln	ggc Gly 840	ctg Leu	atg Met	aac Asn	gtc Val	cag Gln 845	tac Tyr	gca Ala	ctc Leu	aag Lys	gac Asp 850	gac Asp	atc Ile	ctc Leu	2659
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ctg Leu	gac Asp 935	acc Thr	ctg Leu	ctt Leu	tcc Ser	cca Pro 940	gag Glu	atg Met	aag Lys	tcc Ser	act Thr 945	ggc Gly	gag Glu	gtc Val	atg Met	2947
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cgc Arg 1015	aac Asn	ggc Gly	att Ile	gag Glu	tgt Cys	gaa Glu 1020	gtt Val	gtg Val	ctc Leu	aag Lys	gct Ala	tcc Ser	gac Asp	atc Ile	cgc Arg	3187
gaa Glu	ggt Gly	gta Val	gag Glu	ggc Gly	aag Lys	tcc Ser	atc Ile	gtg Val	gat Asp	cgt Arg	atc Ile	cgc Arg	gaa Glu	ggc Gly	gaa Glu	3235

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Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His			
1050	1055	1060	
gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg			3331
Asp Gly Tyr Asp Ile Arg Ala Ala Val Thr Val Gly Val Pro Leu			
1065	1070	1075	
atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc			3379
Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala			
1080	1085	1090	
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Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His			
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Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn			
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Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr			
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Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys			
65	70	75	80
Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly			
85	90	95	
Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile			
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Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile			
115	120	125	
Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile			
130	135	140	
Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val			
145	150	155	160
His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser			
165	170	175	



Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	
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Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	
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Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	
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Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	
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Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	
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Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln	
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Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn	
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Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu	
	290					295					300					
Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	
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Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr	
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Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe	
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Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe	
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Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser	
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Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys	
				405					410					415		
Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val	
			420					425					430			
Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu	
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Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala	Ser	
	450					455						460				
Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe	
465					470					475					480	
Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg	
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
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 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
 545 550 555 560  
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
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 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
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 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
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Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
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Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala
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Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
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Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser
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Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala
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Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
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Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile
			980					985					990		
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&lt;210&gt; 369

&lt;211&gt; 3221

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(3198)

&lt;223&gt; FRXA02234

&lt;400&gt; 369

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct      96
Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
      20              25              30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt      144
Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
      35              40              45

ggt ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc      192
Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
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Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
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Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
      85              90              95

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Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
      100              105              110

gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca      384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
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tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa      432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
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gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca      480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
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gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att      576
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
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gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg      624
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
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gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat      672
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp

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gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala 260 265 270			816
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gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala 405 410 415			1248
tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln 420 425 430			1296
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cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu 450 455 460			1392

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Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu	
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Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp	
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Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu	
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Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu	
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Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	
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Thr	Leu	Gly	Ala	Gln	Asp	Ile	Glu	Lys	Val	Arg	Glu	Ala	Thr	Lys	Lys	
	770					775					780					
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 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
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Ile	Leu	Gly	Ser	Gly	Pro	Asn	Arg	Ile	Gly	Gln	Gly	Ile	Glu	Phe	Asp
530						535					540				
Tyr	Ser	Cys	Val	His	Ala	Ala	Leu	Glu	Leu	Ser	Arg	Val	Gly	Tyr	Glu
545					550					555					560
Thr	Val	Met	Val	Asn	Cys	Asn	Pro	Glu	Thr	Val	Ser	Thr	Asp	Tyr	Asp
				565					570					575	
Thr	Ala	Asp	Arg	Leu	Tyr	Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met
			580					585						590	
Glu	Val	Tyr	His	Ala	Glu	Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile
		595					600						605		
Val	Gln	Leu	Gly	Gly	Gln	Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys
	610					615					620				
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met
625					630					635					640
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
				645					650					655	
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
			660					665						670	
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val
		675					680					685			
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu
	690					695					700				
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu
705					710					715					720
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu
				725					730					735	
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu
			740					745					750		
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met
		755					760					765			

Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys  
 770 775 780  
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala  
 785 790 795 800  
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser  
 805 810 815  
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys  
 820 825 830  
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp  
 835 840 845  
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp  
 850 855 860  
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg  
 865 870 875 880  
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
 885 890 895  
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
 900 905 910  
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
 915 920 925  
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
 930 935 940  
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
 945 950 955 960  
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
 965 970 975  
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
 980 985 990  
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
 995 1000 1005  
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val  
 1010 1015 1020  
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
 1025 1030 1035 1040  
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala  
 1045 1050 1055  
 Leu Gln Glu Leu Asp His Ala Val Lys Ala  
 1060 1065

&lt;210&gt; 371

&lt;211&gt; 1389

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; RXS02565

&lt;400&gt; 371

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ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttacgacga 60
aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
                                         Val Asn Asp Leu Thr
                                         1                               5

cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
                        10                        15                        20

ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
                        25                        30                        35

ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
                        40                        45                        50

gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
                        55                        60                        65

cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
                        70                        75                        80                        85

att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
                        90                        95                        100

gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
                        105                        110                        115

ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
                        120                        125                        130

gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
                        135                        140                        145

tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
                        150                        155                        160                        165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643
Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
                        170                        175                        180

att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg

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185								190				195					
gac	agc	gct	att	gtc	aag	atc	ggc	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
		200				205				210							
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
		215				220				225							
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
		230				235				240				245			
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
				250				255						260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggc	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
		265						270				275					
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280				285						290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct	1027	
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
		295				300				305							
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct	1075	
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
310				315						320				325			
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg	1123	
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
				330				335						340			
gaa	aaa	gtt	ctt	ggc	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att	1171	
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
		345				350						355					
att	tcc	tct	ggc	ggc	tct	gac	ctg	cgc	ttt	ggc	cgt	cga	cta	ggc	ggc	1219	
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
		360				365						370					
gtt	ggc	tat	ggc	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa	1267	
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu		
		375				380				385							
gca	atg	ggg	caa	ctt	cac	tcc	cat	gac	gag	gcg	ctg	tac	ctg	gaa	gat	1315	
Ala	Met	Gly	Gln	Leu	His	Ser	His	Asp	Glu	Ala	Leu	Tyr	Leu	Glu	Asp		
390				395						400				405			
ctt	gaa	ctg	act	gtt	cgg	ggc	tat	gac	tcc	gtc	gtg	cgt	gaa	ttc	cta	1363	
Leu	Glu	Leu	Thr	Val	Arg	Gly	Tyr	Asp	Ser	Val	Val	Arg	Glu	Phe	Leu		
				410				415						420			
ggc	taaaaacatg					aagcaggagt		ctt								1389	
Gly																	

&lt;210&gt; 372

&lt;211&gt; 422

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu  
 1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
 20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
 35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
 50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
 65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
 85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
 100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
 115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
 130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
 145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
 165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
 180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220

Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240

Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255

Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270

Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285

Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

&lt;210&gt; 373

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(502)

&lt;223&gt; RXS02937

&lt;400&gt; 373

gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60

tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163  
 Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met  
 10 15 20

gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211  
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val  
 25 30 35

gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259  
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His  
 40 45 50

gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307  
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser  
 55 60 65

cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355  
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala  
 70 75 80 85

gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403  
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala  
 90 95 100

ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451  
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu  
 105 110 115

gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499  
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val  
 120 125 130

aaa taattggcta atgaatcctt ttc 525  
 Lys

<210> 374  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile  
 1 5 10 15

Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr  
 20 25 30

Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala  
 35 40 45

His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val  
 50 55 60

Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala  
 65 70 75 80

Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala  
 85 90 95

Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp  
 100 105 110

Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala  
 115 120 125

Ser Ala Trp Leu Val Lys  
 130

<210> 375  
 <211> 966  
 <212> DNA  
 <213> Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(943)

&lt;223&gt; RXA02194

&lt;400&gt; 375

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gaaatctccc agctcattta ttggacccag gtcatcatgg ttgctcgcg cctgaagcca 60
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115
                                         Met Leu Lys Ile Ala
                                         1 5
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala
                        10 15 20
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe
                        25 30 35
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile
                        40 45 50
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307
Ala Ile Tyr Val Ala Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg
                        55 60 65
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu
                        70 75 80 85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu
                        90 95 100
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro
                        105 110 115
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val
                        120 125 130
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala
                        135 140 145
gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
                        150 155 160 165
ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
                        170 175 180
gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
                        185 190 195
cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739

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Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
 200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
 215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
 230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
 250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
 265 270 275

atc gcc cgc atc tagttttaac taccctcgaa aat 966  
 Ile Ala Arg Ile  
 280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
 1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
 20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
 35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
 50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
 65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
 85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr

165										170					175				
Ser	Glu	Ala	Val	Ile	Val	Gly	Arg	Lys	Asp	Glu	Lys	Val	Thr	Pro	Glu				
			180					185							190				
Gln	Gln	Ile	Leu	Leu	Arg	Arg	Ile	Gln	Gly	Ile	Leu	His	Ala	Gln	Asn				
		195					200					205							
Phe	Leu	Met	Leu	Asp	Tyr	Asn	Val	Asp	Arg	Asp	Asn	Leu	Asp	Ala	Ala				
	210					215					220								
Thr	Ala	Val	Thr	Pro	Gly	Leu	Ser	Gly	Pro	Thr	Val	Ser	Pro	Leu	Ala				
225					230					235					240				
Arg	Asp	Asn	Trp	Val	Ala	Val	Arg	Ala	Met	Val	Pro	Arg	Arg	Ser	Ala				
			245						250					255					
Asn	Ala	Ile	Met	Asp	Lys	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Ala	Ile	Leu				
		260						265						270					
Ala	Ser	Glu	Ile	Arg	Ile	Ala	Arg	Ile											
		275					280												

&lt;210&gt; 377

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(370)

&lt;223&gt; RXA02195

&lt;400&gt; 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccc	aacacacatt	gataactgtt		gtgtggaaga		atg	tac	cga	gtg	aag	115
						Met	Tyr	Arg	Val	Lys	
						1				5	

aca	ttt	gac	tcg	ctg	tac	gaa	gaa	ctt	ctt	aac	cgt	gct	cag	acc	cgc	163
Thr	Phe	Asp	Ser	Leu	Tyr	Glu	Glu	Leu	Leu	Asn	Arg	Ala	Gln	Thr	Arg	
				10					15					20		

cct	gaa	ggg	tct	gga	acc	gtg	gcc	gcc	ttg	gat	aaa	ggc	atc	cat	cat	211
Pro	Glu	Gly	Ser	Gly	Thr	Val	Ala	Ala	Leu	Asp	Lys	Gly	Ile	His	His	
			25					30					35			

cta	ggt	aag	aag	gtc	atc	gaa	gaa	gcc	gga	gag	gtc	tgg	att	gca	gcc	259
Leu	Gly	Lys	Lys	Val	Ile	Glu	Glu	Ala	Gly	Glu	Val	Trp	Ile	Ala	Ala	
		40						45				50				

gag	tat	gag	acc	gat	gaa	gag	cta	gcc	gga	gaa	atc	tcc	cag	ctc	att	307
Glu	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Ala	Gly	Glu	Ile	Ser	Gln	Leu	Ile	
	55					60					65					

tat	tgg	acc	cag	gtc	atc	atg	gtt	gct	cgc	ggc	ctg	aag	cca	gaa	gat	355
Tyr	Trp	Thr	Gln	Val	Ile	Met	Val	Ala	Arg	Gly	Leu	Lys	Pro	Glu	Asp	
	70				75					80					85	

atc tac aag aac ctg taggagtttt aaagcaatca tgt  
 Ile Tyr Lys Asn Leu  
 90

393

&lt;210&gt; 378

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn  
 1 5 10 15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp  
 20 25 30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu  
 35 40 45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu  
 50 55 60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly  
 65 70 75 80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu  
 85 90

&lt;210&gt; 379

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(454)

&lt;223&gt; RXA01097

&lt;400&gt; 379

gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaagggagc cattaagat gcaggatttg aggtgcgga atg agt gac aat cca 115  
 Met Ser Asp Asn Pro  
 1 5

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
 10 15 20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
 25 30 35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
 40 45 50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp

55	60	65	
atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc			355
Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala			
70	75	80	85
ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc			403
Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly			
	90	95	100
ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg			451
Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu			
	105	110	115
ctg taaaagcaac aacgattaag gaa			477
Leu			

<210> 380  
 <211> 118  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 380  
 Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
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 Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
 20 25 30  
 Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
 35 40 45  
 Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
 50 55 60  
 Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
 65 70 75 80  
 Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
 85 90 95  
 Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
 100 105 110  
 Asp Asn Asp Val Leu Leu  
 115

<210> 381  
 <211> 861  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(838)  
 <223> RXA01100

<400> 381

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aaactggatc aactacatct aacagatagg atcaatatcc atg acc ttc act att 115  
Met Thr Phe Thr Ile  
1 5

ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163  
Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln  
10 15 20

ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211  
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala  
25 30 35

ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259  
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu  
40 45 50

gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307  
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile  
55 60 65

gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355  
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp  
70 75 80 85

gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403  
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn  
90 95 100

att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451  
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile  
105 110 115

caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499  
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu  
120 125 130

gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547  
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly  
135 140 145

gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595  
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg  
150 155 160 165

ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643  
Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
170 175 180

gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
185 190 195

gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
200 205 210

tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
215 220 225

gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
 230 235 240 245

ggt taatacatgg atgctcgtgg gat 861  
 Gly

<210> 382

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
 1 5 10 15

Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30

Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45

His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60

Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80

Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95

Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110

Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125

Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140

Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160

Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr  
 165 170 175

Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr  
 180 185 190

Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val  
 195 200 205

Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile  
 210 215 220

Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala  
 225 230 235 240

Ala Val Glu Lys Leu Gly  
245

<210> 383  
<211> 756  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(733)  
<223> RXA01101

<400> 383  
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cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115  
Met Thr Lys Thr Val  
1 5  
gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163  
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala  
10 15 20  
cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211  
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val  
25 30 35  
tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259  
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp  
40 45 50  
gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307  
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly  
55 60 65  
cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355  
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met  
70 75 80 85  
cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403  
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly  
90 95 100  
tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451  
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu  
105 110 115  
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg 499  
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met  
120 125 130  
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat 547  
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr  
135 140 145  
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca 595  
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro  
150 155 160 165



gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg 643  
 Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val  
                   170                  175                  180

gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt 691  
 Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly  
                   185                  190                  195

gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc 733  
 Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile  
                   200                  205                  210

taacagatag gatcaatatt cat 756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg  
   1                  5                  10                  15

Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser  
                   20                  25                  30

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly  
                   35                  40                  45

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly  
   50                  55                  60

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly  
   65                  70                  75                  80

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly  
                   85                  90                  95

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu  
                   100                  105                  110

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro  
                   115                  120                  125

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr  
                   130                  135                  140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
   145                  150                  155                  160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
                   165                  170                  175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
                   180                  185                  190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
                   195                  200                  205

Asn Tyr Ile

210

&lt;210&gt; 385

&lt;211&gt; 723

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXN01657

&lt;400&gt; 385

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cctccgcatc tgccgacgta tcccgcggcc tgggtgaagc catgggtgggc atcaacgtat 60
ccgacgttcc agcaccacac cgactcgccg agcgcgggctg gtg atc gtt gga gtt 115
                                         Val Ile Val Gly Val
                                         1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
                        10                        15                        20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
                        25                        30                        35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
                        40                        45                        50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
                        55                        60                        65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
                        70                        75                        80                        85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
                        90                        95                        100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
                        105                        110                        115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
                        120                        125                        130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
                        135                        140                        145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
150                        155                        160                        165

caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643

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Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
 170 175 180  
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
 185 190 195  
 ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
 200

<210> 386  
 <211> 200  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 386  
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15  
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160  
 Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro  
 165 170 175  
 Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val  
 180 185 190  
 Arg Lys His Ala Glu Leu Ala Ile  
 195 200

<210> 387  
 <211> 601  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(601)

&lt;223&gt; FRXA01657

&lt;400&gt; 387

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ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
                                   Val Ile Val Gly Val
                                   1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
                                   10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
                                   25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
                                   40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
                                   55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
                                   70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
                                   90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
                                   105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
                                   120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
                                   135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
                                   150 155 160 165

caa ggc
Gln Gly 601

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&lt;210&gt; 388

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 388

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly  
 165

&lt;210&gt; 389

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA01098

&lt;400&gt; 389

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gcaggtaatg accagtcgtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115  
 Met Gly Val Ala Ile  
 1 5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163  
 Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly  
 10 15 20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211  
 Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala

25	30	35	
aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val 40 45 50			259
acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg 55 60 65			307
acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg 70 75 80 85			355
agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val 90 95 100			403
tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu 105 110 115			451
tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg 120 125 130			499
cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr 135 140 145			547
acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala 150 155 160 165			595
aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met 170 175 180			643
gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys 185 190 195			691
gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly 200 205 210			739
aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val 215 220 225			787
ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val 230 235 240 245			835
aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys 250 255			884
tccacaagag tat			897

&lt;210&gt; 390

&lt;211&gt; 258

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 390

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Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
 245 250 255

Arg Lys

&lt;210&gt; 391

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; RXN01104

&lt;400&gt; 391

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Met Thr Val Ala Pro
1 5
aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20
gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35
cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50
gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65
acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85
att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100
atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115
tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130
ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145
gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165
gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
170 175 180
ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
185 190 195

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act aag gga gcg ctc tagacatgaa ctcttctccc atc  
 Thr Lys Gly Ala Leu  
 200

729

&lt;210&gt; 392

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
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Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
 195 200

&lt;210&gt; 393

&lt;211&gt; 729

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; FRXA01104



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Val	His	Gly	Ser	Phe	Asp	Leu	Lys	Val	His	Ala	Lys	Gly	Asp	Ile	Glu
	50					55					60				
Ile	Asp	Ala	His	His	Thr	Val	Glu	Asp	Thr	Ala	Ile	Val	Leu	Gly	Gln
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Ala	Leu	Leu	Asp	Ala	Ile	Gly	Asp	Lys	Lys	Gly	Ile	Arg	Arg	Phe	Ala
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Ser	Cys	Gln	Leu	Pro	Met	Asp	Glu	Ala	Leu	Val	Glu	Ser	Val	Val	Asp
			100					105					110		
Ile	Ser	Gly	Arg	Pro	Tyr	Phe	Val	Ile	Ser	Gly	Glu	Pro	Asp	His	Met
		115					120					125			
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	130				135						140				
Phe	Phe	Glu	Thr	Leu	Ala	Leu	Asn	Ser	Arg	Ile	Thr	Leu	His	Val	Ile
145					150					155					160
Cys	His	Tyr	Gly	Arg	Asp	Pro	His	His	Ile	Thr	Glu	Ala	Glu	Tyr	Lys
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Ala	Val	Ala	Arg	Ala	Leu	Arg	Gly	Ala	Val	Glu	Met	Asp	Pro	Arg	Gln
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<222> (101)..(964)
<223> RXN00446
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Met Gly Ala Val Glu

ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val	
				10					15					20		
acg	gta	ggg	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala	
				25					30					35		
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu	
				40					45					50		
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile	
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ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala	
				70					75					80		
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro	
				90					95					100		
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys	
				105					110					115		
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe	
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aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His	
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gac	aac	gtg	att	ggg	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala	
				150					155					160		
ggc	ttg	cgt	gtt	ggg	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala	
				170					175					180		
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala	
				185					190					195		
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val	
				200					205					210		
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggg	gct	787
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala	
				215					220					225		
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala	
				230					235					240		
														245		

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 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
                   250                  255                  260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
                   265                  270                  275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgcgg 984  
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tgc 987

<210> 396

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 396

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                   20                  25                  30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
                   35                  40                  45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
                   50                  55                  60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
                   65                  70                  75                  80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
                   85                  90                  95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
                   100                  105                  110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
                   115                  120                  125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
                   130                  135                  140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
                   145                  150                  155                  160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                   165                  170                  175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                   180                  185                  190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                   195                  200                  205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

<210> 397  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1) .. (522)  
 <223> FRXA00446

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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
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tagtcctttgg cgttttgcgg tgc 545

<210> 398

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

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 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
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Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 399

<211> 1221

<212> DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1198)

&lt;223&gt; RXA01105

&lt;400&gt; 399

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                                         Met Thr Lys Ile Thr
                                         1           5

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Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
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ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
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cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
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Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
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gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
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Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
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Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
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gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
                        120                        125                        130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
                        135                        140                        145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
                        150                        155                        160                        165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
                        170                        175                        180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
                        185                        190                        195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739

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Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Thr	Leu	Leu		
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Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	Thr	Met	Ser	Lys	Ala		
	215					220					225						
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Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	Val	Ala	Asn	Pro	Ala		
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Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	Tyr	His	Leu	Ser	Ala		
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ctg	agc	caa	gca	gcc	gca	atc	gta	gcg	ctg	cgt	cac	tcc	gct	gac	acg	931	
Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	His	Ser	Ala	Asp	Thr		
			265					270					275				
ctg	gga	acc	gtc	gaa	aag	ctc	tct	gta	gag	cgt	gtt	cgc	gtg	gca	gca	979	
Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	Val	Arg	Val	Ala	Ala		
		280						285					290				
cgc	ttg	gag	gaa	ctg	ggc	tac	gct	gtg	gtt	cca	agt	gag	tcc	aac	ttt	1027	
Arg	Leu	Glu	Glu	Leu	Gly	Tyr	Ala	Val	Val	Pro	Ser	Glu	Ser	Asn	Phe		
	295					300					305						
gtg	ttc	ttt	gga	gat	ttc	tcc	gat	cag	cac	gcg	gca	tgg	cag	gca	ttt	1075	
Val	Phe	Phe	Gly	Asp	Phe	Ser	Asp	Gln	His	Ala	Ala	Trp	Gln	Ala	Phe		
310					315					320					325		
ttg	gat	agg	gga	gtg	ctc	atc	cgc	gat	gtg	gga	atc	gct	ggg	cac	ttg	1123	
Leu	Asp	Arg	Gly	Val	Leu	Ile	Arg	Asp	Val	Gly	Ile	Ala	Gly	His	Leu		
				330					335					340			
cgc	act	acc	att	ggt	gtg	cct	gag	gaa	aat	gat	gcg	ttt	ttg	gac	gca	1171	
Arg	Thr	Thr	Ile	Gly	Val	Pro	Glu	Glu	Asn	Asp	Ala	Phe	Leu	Asp	Ala		
			345					350					355				
gct	gca	gag	atc	atc	aag	ctg	aac	ctg	taagagagaa	gaatttttca						1218	
Ala	Ala	Glu	Ile	Ile	Lys	Leu	Asn	Leu									
		360				365											
tga																	1221
<210> 400																	
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<212> PRT																	
<213> Corynebacterium glutamicum																	
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Met	Thr	Lys	Ile	Thr	Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg		
1				5					10					15			
Gly	Glu	His	Ala	Tyr	Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu		
			20					25					30				
Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp		
		35					40					45					

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
 50 55 60  
 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
 65 70 75 80  
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
 85 90 95  
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
 100 105 110  
 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
 115 120 125  
 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
 130 135 140  
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
 145 150 155 160  
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
 165 170 175  
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
 180 185 190  
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
 195 200 205  
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
 210 215 220  
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
 225 230 235 240  
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
 245 250 255  
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
 260 265 270  
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320  
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335  
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350  
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

cDNA sequence																	Position	
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aagaatt	ttcgc	attca	acctt	ttaag	gggaga	acttt	tcgcc	atg	ttg	aat	gtc	act					115	
												Met	Leu	Asn	Val	Thr	5	
												1						
gac	ctg	cga	ggt	caa	aca	cca	tcc	aag	agc	gac	atc	cga	cgt	gct	ttg	163		
Asp	Leu	Arg	Gly	Gln	Thr	Pro	Ser	Lys	Ser	Asp	Ile	Arg	Arg	Ala	Leu	20		
												10	15					
cca	cgt	ggt	ggc	act	gac	gtg	tgg	tct	gtg	ctt	ccc	ata	gtg	cag	cct	211		
Pro	Arg	Gly	Gly	Thr	Asp	Val	Trp	Ser	Val	Leu	Pro	Ile	Val	Gln	Pro	35		
												25	30					
gtt	gta	gaa	gat	gtc	caa	aac	cgc	ggc	gct	gaa	gct	gct	ttg	gat	tac	259		
Val	Val	Glu	Asp	Val	Gln	Asn	Arg	Gly	Ala	Glu	Ala	Ala	Leu	Asp	Tyr	50		
												40	45					
ggc	gag	aag	ttc	gac	cat	att	cgc	ccc	gcc	tcg	gtg	cgg	gtg	cca	gct	307		
Gly	Glu	Lys	Phe	Asp	His	Ile	Arg	Pro	Ala	Ser	Val	Arg	Val	Pro	Ala	65		
												55	60					
gag	gtt	att	gct	gca	gca	gaa	aac	acc	tta	gat	ccg	ttg	gtg	cgt	gaa	355		
Glu	Val	Ile	Ala	Ala	Ala	Glu	Asn	Thr	Leu	Asp	Pro	Leu	Val	Arg	Glu	85		
												70	75					
tcg	att	gaa	gag	tcg	att	cgt	cgc	gtc	cgc	aag	gtt	cac	gct	gag	caa	403		
Ser	Ile	Glu	Glu	Ser	Ile	Arg	Arg	Val	Arg	Lys	Val	His	Ala	Glu	Gln	100		
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aag	cca	tcc	gag	cac	acc	act	gaa	ctt	tca	cca	ggt	ggc	acc	gtc	act	451		
Lys	Pro	Ser	Glu	His	Thr	Thr	Glu	Leu	Ser	Pro	Gly	Gly	Thr	Val	Thr	115		
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gag	cgt	ttc	atg	ccg	att	gat	cgc	gtg	gga	ctg	tac	gtt	cca	ggc	ggc	499		
Glu	Arg	Phe	Met	Pro	Ile	Asp	Arg	Val	Gly	Leu	Tyr	Val	Pro	Gly	Gly	130		
												120	125					
aat	gcg	gtg	tac	cca	tca	agc	gtg	att	atg	aat	act	gtc	cca	gct	caa	547		
Asn	Ala	Val	Tyr	Pro	Ser	Ser	Val	Ile	Met	Asn	Thr	Val	Pro	Ala	Gln	145		
												135	140					
gag	gct	ggt	gtg	aac	tcc	ctt	gtg	gtt	gcg	tcg	cct	cct	cag	gct	gag	595		
Glu	Ala	Gly	Val	Asn	Ser	Leu	Val	Val	Ala	Ser	Pro	Pro	Gln	Ala	Glu	165		
												150	155					
cac	ggt	ggc	tgg	cct	cac	ccc	acc	att	ttg	gcg	gcg	tgt	tcc	atc	ttg	643		
His	Gly	Gly	Trp	Pro	His	Pro	Thr	Ile	Leu	Ala	Ala	Cys	Ser	Ile	Leu	180		
												170	175					

ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	
330 335 340	
cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc	1171
Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly	
345 350 355	
gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac	1219
Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His	
360 365 370	
gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg	1267
Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr	
375 380 385	
cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct	1315
His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala	
390 395 400 405	
ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat	1363
Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp	
410 415 420	
ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc	1411

Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435

acc acc gac gag gcc taagaaaaat gaccaaatt act  
 Thr Thr Asp Glu Ala  
 440

1449

&lt;210&gt; 402

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp  
 1 5 10 15

Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
 20 25 30

Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45

Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60

Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80

Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro  
 100 105 110

Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu  
 115 120 125

Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn  
 130 135 140

Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser  
 145 150 155 160

Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala  
 165 170 175

Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly  
 180 185 190

Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu  
 195 200 205

Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala  
 210 215 220

Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro  
 225 230 235 240

Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val  
 245 250 255

Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser  
 260 265 270

Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu  
 275 280 285

Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu  
 290 295 300

Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser  
 305 310 315 320

Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile  
 325 330 335

His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly  
 340 345 350

Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser  
 355 360 365

Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser  
 370 375 380

Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu  
 385 390 395 400

Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe  
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

&lt;210&gt; 403

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXC00930

&lt;400&gt; 403

acggcgccacc acacatttgg tggtgtattg agctatctct gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg

25	30	35	
aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile 40 45 50			259
aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala 55 60 65			307
cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn 70 75 80 85			355
atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu 90 95 100			403
tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala 105 110 115			451
atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr 120 125 130			499
atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser 135 140 145			547
gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val 150 155 160 165			595
aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile 170 175 180			643
cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp 185 190 195			691
tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp 200 205 210			739
ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp 215 220 225			787
gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu 230 235 240 245			835
aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg Thr Glu Leu Glu Asn Asp 250			876

&lt;210&gt; 404

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

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Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
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Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
          20             25             30

Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
          35             40             45

Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
  50             55             60

Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
  65             70             75             80

Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
          85             90             95

Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
          100             105             110

Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
          115             120             125

Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
          130             135             140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
          145             150             155             160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
          165             170             175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
          180             185             190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
          195             200             205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
          210             215             220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
          225             230             235             240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
          245             250

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&lt;210&gt; 405

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(547)



&lt;223&gt; RXC01096

&lt;400&gt; 405

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gttttgcgtgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
 Met Lys Pro Arg Val  
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp  
 90 95 100

gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag 451  
 Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys  
 105 110 115

gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc 499  
 Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr  
 120 125 130

acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta 547  
 Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu  
 135 140 145

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu  
 1 5 10 15

Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe  
 20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp  
 35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala  
 50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile  
 65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu  
 85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly  
 100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala  
 115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met  
 130 135 140

Ile Gly Cys Ala Leu  
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<210> 407  
 <211> 1020  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(997)  
 <223> RXC01656

<400> 407  
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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115  
 Met Thr Glu Thr Gln  
 1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163  
 Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met  
 10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211  
 Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg  
 25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259  
 Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val  
 40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307  
 Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro  
 55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355  
 Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala  
 70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403  
 Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu

90										95					100					
ggt	ggt	gat	ttc	atc	gac	gag	tcc	gaa	ggt	ctc	agc	cct	gcc	gac	tac	451				
Gly	Val	Asp	Phe	Ile	Asp	Glu	Ser	Glu	Val	Leu	Ser	Pro	Ala	Asp	Tyr					
			105						110			115								
acg	cac	cac	atc	aac	aag	tgg	aag	ttc	gac	ggt	cct	ttc	gtc	tgt	ggc	499				
Thr	His	His	Ile	Asn	Lys	Trp	Lys	Phe	Asp	Val	Pro	Phe	Val	Cys	Gly					
			120						125			130								
gcg	acc	aac	ctc	ggc	gaa	gct	ttg	cga	cgc	atc	acc	gaa	ggc	gct	gca	547				
Ala	Thr	Asn	Leu	Gly	Glu	Ala	Leu	Arg	Arg	Ile	Thr	Glu	Gly	Ala	Ala					
			135						140			145								
atg	atc	cgt	tcc	aag	ggc	gaa	gcc	ggc	acc	ggc	gat	gtc	tct	gaa	gct	595				
Met	Ile	Arg	Ser	Lys	Gly	Glu	Ala	Gly	Thr	Gly	Asp	Val	Ser	Glu	Ala					
			150						155			160			165					
gtc	cgt	cac	ctg	cgc	acc	atc	cgc	ggc	gac	atc	aat	cgc	ctg	cgc	tcc	643				
Val	Arg	His	Leu	Arg	Thr	Ile	Arg	Gly	Asp	Ile	Asn	Arg	Leu	Arg	Ser					
			170						175			180								
ctg	gat	gag	gat	gaa	ctc	ttc	gtc	gcc	gcc	aag	gaa	ttc	cag	gca	cca	691				
Leu	Asp	Glu	Asp	Glu	Leu	Phe	Val	Ala	Ala	Lys	Glu	Phe	Gln	Ala	Pro					
			185						190			195								
tac	gac	ctg	gtc	cgc	gaa	gtc	gcc	tcc	acc	ggc	aag	ctc	cct	gtg	gtc	739				
Tyr	Asp	Leu	Val	Arg	Glu	Val	Ala	Ser	Thr	Gly	Lys	Leu	Pro	Val	Val					
			200						205			210								
acc	ttc	ggt	gca	ggt	ggc	gtc	gca	acc	cca	gcc	gac	gct	gca	ctc	gtg	787				
Thr	Phe	Val	Ala	Gly	Gly	Val	Ala	Thr	Pro	Ala	Asp	Ala	Ala	Leu	Val					
			215						220			225								
cgc	caa	atg	ggc	gcc	gaa	ggc	gtc	ttt	gtc	ggc	tcc	ggc	atc	ttc	aaa	835				
Arg	Gln	Met	Gly	Ala	Glu	Gly	Val	Phe	Val	Gly	Ser	Gly	Ile	Phe	Lys					
			230						235			240			245					
tcc	ggc	aat	cca	gcc	gcc	cgc	gcc	gca	gcg	atc	gtc	aag	gct	gca	acg	883				
Ser	Gly	Asn	Pro	Ala	Ala	Arg	Ala	Ala	Ala	Ile	Val	Lys	Ala	Ala	Thr					
			250						255			260								
ctt	ttc	gac	gac	ccc	tcc	gtc	att	gcc	gac	gta	tcc	cgc	ggc	ctg	ggt	931				
Leu	Phe	Asp	Asp	Pro	Ser	Val	Ile	Ala	Asp	Val	Ser	Arg	Gly	Leu	Gly					
			265						270			275								
gaa	gcc	atg	gtg	ggc	atc	aac	gta	tcc	gac	ggt	cca	gca	cca	cac	cga	979				
Glu	Ala	Met	Val	Gly	Ile	Asn	Val	Ser	Asp	Val	Pro	Ala	Pro	His	Arg					
			280						285			290								
ctc	gcc	gag	cgc	ggc	tgg	tgatcgttgg	agtttttagct	ctc								1020				
Leu	Ala	Glu	Arg	Gly	Trp															
			295																	

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg  
 1 5 10 15  
 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30  
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45  
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60  
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80  
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95  
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110  
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125  
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140  
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160  
 Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile  
 165 170 175  
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys  
 180 185 190  
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly  
 195 200 205  
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala  
 210 215 220  
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly  
 225 230 235 240  
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile  
 245 250 255  
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val  
 260 265 270  
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val  
 275 280 285  
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp  
 290 295

&lt;210&gt; 409

&lt;211&gt; 1065

&lt;212&gt; DNA

$\langle 220 \rangle$ 

$\langle 222 \rangle$  (101) . . (1042)

<223> RXC01158

<400> 409

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agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag 115  
Met Ser Ile Val Glu  
1 5

cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163  
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile  
 10 15 20

ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211  
Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp  
25 30 35

cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259  
Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu  
40 45 50

cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307  
Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu  
55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg 355  
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala  
70 75 80 85

gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg 403  
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu  
90 95 100

tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc 451  
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr  
105 110 115

gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt 499  
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val  
120 125 130

ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att 547  
 Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile  
 135 140 145

ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga 595  
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly  
150 155 160 165

ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca 643  
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro  
170 175 180

ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc 691  
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala  
185 190 195

att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct 739  
 Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala  
 200 205 210

gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg 787  
 Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala  
 215 220 225

ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc 835  
 Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe  
 230 235 240 245

aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat 883  
 Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp  
 250 255 260

gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct 931  
 Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala  
 265 270 275

cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg 979  
 Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu  
 280 285 290

aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac 1027  
 Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp  
 295 300 305

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta 1065  
 Phe Gly Asp Val Leu  
 310

&lt;210&gt; 410

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile  
 1 5 10 15

Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr  
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
 115 120 125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
 130 135 140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Leu Thr Gly  
 145 150 155 160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
 165 170 175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
 180 185 190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
 195 200 205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
 210 215 220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
 225 230 235 240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
 245 250 255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala  
 260 265 270  
 Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu  
 275 280 285  
 Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys  
 290 295 300  
 Pro Gly Arg Ala Asp Phe Gly Asp Val Leu  
 305 310

&lt;210&gt; 411

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1390)

&lt;223&gt; RXA02458

&lt;400&gt; 411

ttgcggagcc acgactgatc ggtcaagtgc tatctcggtt gcatcaataa gcgaatcacc 60

 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115  
 Met Val Phe Val Ser  
 1 5

 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163  
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly  
 10 15 20

ccc	ata	gtc	tcg	gac	ctg	gct	atc	cct	ggg	tcc	aag	tcg	atc	acc	aac	211
Pro	Ile	Val	Ser	Asp	Leu	Ala	Ile	Pro	Gly	Ser	Lys	Ser	Ile	Thr	Asn	
			25					30					35			
cgc	gcc	ctc	atc	ttg	gct	gcg	ctc	gca	tca	act	cca	tcc	acc	atc	att	259
Arg	Ala	Leu	Ile	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Pro	Ser	Thr	Ile	Ile	
		40					45					50				
gat	gtc	ctt	cgt	agt	cgt	gat	acc	gat	ctc	atg	act	gat	ggg	cta	cgc	307
Asp	Val	Leu	Arg	Ser	Arg	Asp	Thr	Asp	Leu	Met	Thr	Asp	Gly	Leu	Arg	
		55				60					65					
agc	ctc	gga	atc	acc	att	act	gaa	gag	gca	gtc	gat	cgc	tac	cgc	gtt	355
Ser	Leu	Gly	Ile	Thr	Ile	Thr	Glu	Glu	Ala	Val	Asp	Arg	Tyr	Arg	Val	
	70				75				80						85	
gag	ccc	gga	cag	ttg	tct	gct	ggc	tcc	gtt	gag	tgt	ggg	ctt	gct	ggg	403
Glu	Pro	Gly	Gln	Leu	Ser	Ala	Gly	Ser	Val	Glu	Cys	Gly	Leu	Ala	Gly	
			90					95						100		
acg	gtc	atg	cgc	ttt	ttg	cct	cct	gtt	gct	gct	ttc	gct	gat	ggg	cct	451
Thr	Val	Met	Arg	Phe	Leu	Pro	Pro	Val	Ala	Ala	Phe	Ala	Asp	Gly	Pro	
			105					110					115			
gtt	cat	ttt	gat	ggc	gat	cct	caa	gct	cgt	gtt	cgt	ccg	atg	acc	agc	499
Val	His	Phe	Asp	Gly	Asp	Pro	Gln	Ala	Arg	Val	Arg	Pro	Met	Thr	Ser	
		120					125					130				
att	ttg	gat	gcg	ctg	cgt	tcg	ctt	ggg	gtg	gag	gta	gac	aac	aac	aat	547
Ile	Leu	Asp	Ala	Leu	Arg	Ser	Leu	Gly	Val	Glu	Val	Asp	Asn	Asn	Asn	
		135				140					145					
ctg	cct	ttc	act	gtt	aat	gct	ggg	gag	gtc	cct	gag	ggg	ggc	gtg	gtt	595
Leu	Pro	Phe	Thr	Val	Asn	Ala	Gly	Glu	Val	Pro	Glu	Gly	Gly	Val	Val	
	150				155				160					165		
gag	att	gat	gct	tcc	ggc	tca	tct	cag	ttt	gtt	tct	ggg	ctt	ttg	ctt	643
Glu	Ile	Asp	Ala	Ser	Gly	Ser	Ser	Gln	Phe	Val	Ser	Gly	Leu	Leu	Leu	
			170					175						180		
tca	gcg	cct	cgt	ttt	aaa	aat	ggc	gtc	acc	gtt	aag	cac	gtc	ggg	ggg	691
Ser	Ala	Pro	Arg	Phe	Lys	Asn	Gly	Val	Thr	Val	Lys	His	Val	Gly	Gly	
			185					190					195			
cgt	ctg	ccg	agc	atg	ccg	cat	att	gag	atg	acc	gtc	gat	atg	ctt	cgt	739
Arg	Leu	Pro	Ser	Met	Pro	His	Ile	Glu	Met	Thr	Val	Asp	Met	Leu	Arg	
		200					205					210				
tcc	gca	ggc	att	gag	atc	gaa	gag	tca	gaa	aat	cag	tgg	gtt	gtt	cat	787
Ser	Ala	Gly	Ile	Glu	Ile	Glu	Glu	Ser	Glu	Asn	Gln	Trp	Val	Val	His	
	215					220				225						
cct	ggg	gag	atc	ttg	ggg	cgg	acc	tgg	cgc	att	gag	ccg	gat	ctt	tct	835
Pro	Gly	Glu	Ile	Leu	Gly	Arg	Thr	Trp	Arg	Ile	Glu	Pro	Asp	Leu	Ser	
	230				235					240				245		
aat	gcg	act	ccg	ttc	cta	gct	gcc	gct	gcg	gtc	act	ggg	gga	acc	atc	883
Asn	Ala	Thr	Pro	Phe	Leu	Ala	Ala	Ala	Ala	Val	Thr	Gly	Gly	Thr	Ile	
			250					255						260		
aag	att	aac	cac	tgg	cca	atc	aaa	act	act	cag	cct	ggc	gat	gct	att	931



Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile  
 265 270 275  
 cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag 979  
 Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln  
 280 285 290  
 ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc 1027  
 Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly  
 295 300 305  
 att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg 1075  
 Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala  
 310 315 320 325  
 gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct 1123  
 Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala  
 330 335 340  
 cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag 1171  
 His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu  
 345 350 355  
 atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg 1219  
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
 360 365 370  
 att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat 1267  
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
 375 380 385  
 cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc 1315  
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
 390 395 400 405  
 gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt 1363  
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
 410 415 420  
 gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat 1410  
 Glu Asn Val Trp Glu Glu Met Val Gly  
 425 430  
 ccg 1413

&lt;210&gt; 412

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Met Val Phe Val Ser Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala  
 1 5 10 15

Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser  
 20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
 35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
 50 55 60  
 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
 65 70 75 80  
 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
 85 90 95  
 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
 100 105 110  
 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
 115 120 125  
 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
 130 135 140  
 Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
 180 185 190  
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
 355 360 365  
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp

370 375 380

His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
385 390 395 400

Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
405 410 415

Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
420 425 430

<210> 413  
<211> 1266  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1243)  
<223> RXA02790

<400> 413

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agggaaattt cccaggatga accaaatccg aaaccgcccgg atg gag ccc gtc tac 115  
Met Glu Pro Val Tyr  
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307  
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu  
55 60 65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355  
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser  
70 75 80 85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403  
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln  
90 95 100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451  
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp  
105 110 115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499  
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp  
120 125 130

gtc	act	gtt	gtc	ggc	gga	aac	acc	cgc	gcg	gga	atc	tac	tcc	cag	atc	547
Val	Thr	Val	Val	Gly	Gly	Asn	Thr	Arg	Ala	Gly	Ile	Tyr	Ser	Gln	Ile	
	135					140					145					
gca	gcc	gtg	acc	tgc	acc	gaa	ggc	tcc	gcc	aac	tgc	atc	acc	gct	gag	595
Ala	Ala	Val	Thr	Cys	Thr	Glu	Gly	Ser	Ala	Asn	Cys	Ile	Thr	Ala	Glu	
	150				155					160					165	
gat	ttg	cag	cag	gtt	gcc	tcc	acc	gtg	tcg	cct	gca	gaa	ttg	ggt	gtc	643
Asp	Leu	Gln	Gln	Val	Ala	Ser	Thr	Val	Ser	Pro	Ala	Glu	Leu	Gly	Val	
				170					175						180	
cca	gat	tgg	gca	atc	gct	gct	gtg	gaa	gct	cgc	gga	act	gat	cca	aag	691
Pro	Asp	Trp	Ala	Ile	Ala	Ala	Val	Glu	Ala	Arg	Gly	Thr	Asp	Pro	Lys	
			185					190					195			
cgc	ctc	gaa	ggc	ctg	atc	atg	cct	ggc	caa	tac	gtg	gtg	gat	cca	tcc	739
Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser	
	200						205					210				
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn	
	215					220					225					
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu	
	230				235				240						245	
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala	
			250						255					260		
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu	
			265				270						275			
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggt	ctg	979
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu	
	280					285						290				
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc	1027
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr	
	295					300					305					
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc	1075
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala	
	310				315					320					325	
gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga	1123
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly	
				330				335						340		
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc	1171
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe	
			345					350					355			
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac	1219
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn	
	360						365					370				
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tggt						1266

Ser Gly Val Leu Asp Ser Asn Arg  
375 380

<210> 414

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Met	Glu	Pro	Val	Tyr	Val	Lys	Arg	Arg	Gln	Arg	Phe	Ile	Ala	Val	Thr	1	5	10	15
Ile	Ala	Ser	Leu	Ile	Leu	Ile	Ile	Gly	Ala	Ile	Ile	Tyr	Ile	Gly	Val	20	25	30	
Ala	Thr	Ser	Asn	Arg	Thr	Pro	His	Asp	Tyr	Glu	Gly	Ser	Gly	Asn	Gly	35	40	45	
Val	Val	Gln	Leu	Val	Glu	Ile	Pro	Glu	Gly	Ser	Ser	Ile	Ser	Glu	Leu	50	55	60	
Gly	Pro	Glu	Leu	Glu	Glu	Arg	Asp	Ile	Val	Ala	Thr	Asn	Ser	Ala	Phe	65	70	75	80
Gln	Thr	Ala	Ala	Ser	Asn	Asn	Pro	Asn	Ala	Gly	Ser	Val	Gln	Pro	Gly	85	90	95	
Phe	Tyr	Arg	Leu	Gln	Glu	Gln	Met	Asn	Ala	Ala	Ala	Ala	Val	Ser	Ala	100	105	110	
Leu	Leu	Asp	Pro	Asp	Asn	Gln	Val	Asp	Leu	Leu	Asp	Ile	His	Gly	Gly	115	120	125	
Ala	Thr	Leu	Met	Asp	Val	Thr	Val	Val	Gly	Gly	Asn	Thr	Arg	Ala	Gly	130	135	140	
Ile	Tyr	Ser	Gln	Ile	Ala	Ala	Val	Thr	Cys	Thr	Glu	Gly	Ser	Ala	Asn	145	150	155	160
Cys	Ile	Thr	Ala	Glu	Asp	Leu	Gln	Gln	Val	Ala	Ser	Thr	Val	Ser	Pro	165	170	175	
Ala	Glu	Leu	Gly	Val	Pro	Asp	Trp	Ala	Ile	Ala	Ala	Val	Glu	Ala	Arg	180	185	190	
Gly	Thr	Asp	Pro	Lys	Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	195	200	205	
Val	Val	Asp	Pro	Ser	Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	210	215	220	
Thr	Arg	Ser	Ala	Asn	His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	225	230	235	240
Asp	Ala	Ile	Gly	Leu	Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	245	250	255	
Ile	Glu	Arg	Glu	Ala	Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	260	265	270	

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr  
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp  
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro  
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu  
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

&lt;210&gt; 415

&lt;211&gt; 644

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (621)

&lt;223&gt; RXN00954

&lt;400&gt; 415

gct	gtg	aag	tgg	ttc	gaa	gcg	tcc	aac	ttc	acc	ttc	ctg	ttc	gca	cct	48
Ala	Val	Lys	Trp	Phe	Glu	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Phe	Ala	Pro	
1				5				10					15			
gcg	tac	aac	cct	gcg	att	gcg	cat	gtg	cag	ccg	gtt	cgc	cag	gcg	ctg	96
Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	Val	Arg	Gln	Ala	Leu	
			20					25					30			
aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	ttg	ctg	tcc	ccg	gcg	144
Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	Leu	Leu	Ser	Pro	Ala	
		35					40					45				
cgc	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	gcc	aat	cat	gga	cag	192
Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	Ala	Asn	His	Gly	Gln	
		50				55					60					
ctc	atc	gcc	gag	gtc	ttc	cgc	gag	ttg	ggc	cgt	aca	cgc	gcg	ctt	gtt	240
Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	Thr	Arg	Ala	Leu	Val	
65				70				75						80		
gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	cac	ggc	acc	acc	ttg	288
Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	His	Gly	Thr	Thr	Leu	
				85				90						95		
gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	cat	tac	acc	atc	gag	336
Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	His	Tyr	Thr	Ile	Glu	
			100				105						110			

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
           115                                  120                                  125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
           130                                  135                                  140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
           145                                  150                                  155                                  160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                                   165                                  170                                  175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                                   180                                  185                                  190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
                                   195                                  200                                  205

tagtaataat ctgcccacag tgt 644

<210> 416

<211> 207

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 416

Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro  
           1                                  5                                  10                                  15

Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
                                   20                                  25                                  30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
                                   35                                  40                                  45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
           50                                  55                                  60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
           65                                  70                                  75                                  80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
                                   85                                  90                                  95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
                                   100                                  105                                  110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
           115                                  120                                  125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
           130                                  135                                  140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala

145		150		155		160
Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln						
		165		170		175
Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala						
		180		185		190
Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp						
		195		200		205

&lt;210&gt; 417

&lt;211&gt; 611

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(588)

&lt;223&gt; FRXA00954

&lt;400&gt; 417

ttc ctg ttc gca cct gcg tac aac cct gcg att gcg cat gtg cag ccg	48
Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro	
1 5 10 15	
ggt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca	96
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro	
20 25 30	
ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat	144
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn	
35 40 45	
gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt	192
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg	
50 55 60	
aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc	240
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val	
65 70 75 80	
cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag	288
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu	
85 90 95	
cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt	336
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu	
100 105 110	
gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc	384
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg	
115 120 125	
gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct	432
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala	
130 135 140	
gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg	480
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu	



145	150	155	160	
aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc	528			
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr				
165	170	175		
cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag	576			
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu				
180	185	190		
tct tcc aat gac tagtaataat ctgcccacag tgt	611			
Ser Ser Asn Asp				
195				

&lt;210&gt; 418

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro	
1 5 10 15	
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro	
20 25 30	
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn	
35 40 45	
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg	
50 55 60	
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val	
65 70 75 80	
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu	
85 90 95	
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu	
100 105 110	
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg	
115 120 125	
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala	
130 135 140	
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu	
145 150 155 160	
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr	
165 170 175	
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu	
180 185 190	
Ser Ser Asn Asp	
195	

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<220>
<221> CDS
<222> (101)..(1654)
<223> RXN00957
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aaccggcaag ccctggatcg aatgaagctc gcagcgagta attatttgat gtttcccaga 60

cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
10 15 20

agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259  
 Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
           40                          45                          50

aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307  
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
55 60 65

ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355  
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
70 75 80 85

ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403  
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
90 95 100

gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451  
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
105 110 115

gtg	ctg	cgc	aag	ttg	cag	ttc	gag	tcc	ggt	tac	agc	gac	gcg	tcc	ctg	499
Val	Leu	Arg	Lys	Leu	Gln	Phe	Glu	Ser	Gly	Tyr	Ser	Asp	Ala	Ser	Leu	
		120					125					130				

cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
135 140 145

acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595  
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
150 155 160 165

ttc	gtc	ctc	gcg	gaa	atc	gtc	ctg	gac	atc	aat	cac	cag	gac	cag	acc	643
Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp	Ile	Asn	His	Gln	Asp	Gln	Thr	
				170					175					180		

gcc	aaa	ctc	gcc	ggc	gtc	tcc	aac	gcc	cca	ggc	gag	ctc	gag	gcc	gag	691
Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	Pro	Gly	Glu	Leu	Glu	Ala	Glu	
		185						190					195			
ctc	aac	aag	ctt	tca	ttg	ctt	atc	gac	gcc	gcc	ctc	ccc	gca	acc	gaa	739
Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	Ala	Ala	Leu	Pro	Ala	Thr	Glu	
		200					205					210				
cac	gcc	tac	caa	acc	acc	cct	cac	gac	ggc	gac	act	ctt	cgc	gtt	gtg	787
His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	Gly	Asp	Thr	Leu	Arg	Val	Val	
	215					220					225					
gct	gat	att	ccc	gat	gct	cag	ttc	cgc	acc	cag	atc	aat	gag	ctg	aaa	835
Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	Thr	Gln	Ile	Asn	Glu	Leu	Lys	
230					235				240						245	
gaa	aac	att	tac	aac	ggc	gac	atc	tac	caa	gtt	gtc	ccg	gcg	cgc	act	883
Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	Gln	Val	Val	Pro	Ala	Arg	Thr	
				250					255					260		
ttc	acc	gca	cca	tgt	cct	gat	gca	ttc	gct	gct	tat	ctg	cag	ctg	cgt	931
Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	Ala	Ala	Tyr	Leu	Gln	Leu	Arg	
		265					270						275			
gcc	acc	aac	ccg	tcg	ccg	tac	atg	ttc	tat	atc	cgt	ggc	ctc	aac	gaa	979
Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	Tyr	Ile	Arg	Gly	Leu	Asn	Glu	
		280					285					290				
ggc	cgc	tcc	tat	gaa	ctt	ttt	ggc	gca	tcc	cct	gag	tcc	aac	ctc	aag	1027
Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	Ser	Pro	Glu	Ser	Asn	Leu	Lys	
		295				300					305					
ttc	acc	gct	gct	aac	cgt	gag	ctg	cag	ctg	tac	cca	atc	gca	ggt	acc	1075
Phe	Thr	Ala	Ala	Asn	Arg	Glu	Leu	Gln	Leu	Tyr	Pro	Ile	Ala	Gly	Thr	
310					315					320					325	
cgc	ccc	cgt	gga	ctc	aac	cca	gat	ggc	tcc	atc	aac	gat	gag	cta	gat	1123
Arg	Pro	Arg	Gly	Leu	Asn	Pro	Asp	Gly	Ser	Ile	Asn	Asp	Glu	Leu	Asp	
				330					335					340		
atc	cgc	aat	gag	ttg	gat	atg	cgc	act	gat	gcc	aaa	gag	atc	gcg	gag	1171
Ile	Arg	Asn	Glu	Leu	Asp	Met	Arg	Thr	Asp	Ala	Lys	Glu	Ile	Ala	Glu	
			345					350					355			
cac	acc	atg	ctt	gtc	gat	ctc	gcc	cgc	aac	gac	ctg	gcc	cgc	gtc	tcg	1219
His	Thr	Met	Leu	Val	Asp	Leu	Ala	Arg	Asn	Asp	Leu	Ala	Arg	Val	Ser	
		360					365					370				
gtc	cca	gcg	tcg	cgc	cgg	gtt	gcg	gat	ctt	ttg	cag	gtg	gat	cgc	tat	1267
Val	Pro	Ala	Ser	Arg	Arg	Val	Ala	Asp	Leu	Leu	Gln	Val	Asp	Arg	Tyr	
		375				380					385					
tcc	cgc	gtg	atg	cac	ttg	gtg	tcc	cgt	gtg	acg	gcg	acg	ttg	gac	cca	1315
Ser	Arg	Val	Met	His	Leu	Val	Ser	Arg	Val	Thr	Ala	Thr	Leu	Asp	Pro	
390					395					400					405	
gag	ctt	gat	gct	ttg	gac	gcc	tat	cgg	gcg	tgc	atg	aat	atg	ggc	acg	1363
Glu	Leu	Asp	Ala	Leu	Asp	Ala	Tyr	Arg	Ala	Cys	Met	Asn	Met	Gly	Thr	
				410					415					420		
ttg	acc	ggc	gct	ccg	aag	ttg	cgc	gct	atg	gag	ctg	ttg	cgc	ggc	gtc	1411

Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val  
                   425                                  430                                  435  
  
 gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc 1459  
 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
                   440                                  445                                  450  
  
 ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc 1507  
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
                   455                                  460                                  465  
  
 cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat 1555  
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
                   470                                  475                                  480                                  485  
  
 tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc 1603  
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
                                   490                                  495                                  500  
  
 gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc 1651  
 Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
                                   505                                  510                                  515  
  
 cga tgacacacgt tggttctcatt gat 1677  
 Arg

&lt;210&gt; 420

&lt;211&gt; 518

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu  
   1                                  5                                  10                                  15  
  
 Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp  
                   20                                  25                                  30  
  
 Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
                   35                                  40                                  45  
  
 Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
                   50                                  55                                  60  
  
 Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
                   65                                  70                                  75                                  80  
  
 Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
                                   85                                  90                                  95  
  
 Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
                   100                                  105                                  110  
  
 Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
                   115                                  120                                  125  
  
 Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
                   130                                  135                                  140

Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445  
 Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460  
 Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala

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<210> 421
<211> 1151
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1) .. (1128)
<223> FRXA00957
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<400> 421																
gat	ttc	tta	gaa	acc	ttt	gaa	acg	ctc	ccc	gct	gtc	gag	gag	agc	gtc	48
Asp	Phe	Leu	Glu	Thr	Phe	Glu	Thr	Leu	Pro	Ala	Val	Glu	Glu	Ser	Val	
1				5					10					15		
aac	act	tac	ccc	gat	tac	cag	ttc	gtc	ctc	gcg	gaa	atc	gtc	ctg	gac	96
Asn	Thr	Tyr	Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp	
			20					25					30			
atc	aat	cac	cag	gac	cag	acc	gcc	aaa	ctc	gcc	ggc	gtc	tcc	aac	gcc	144
Ile	Asn	His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala	
			35				40					45				
cca	ggc	gag	ctc	gag	gcc	gag	ctc	aac	aag	ctt	tca	ttg	ctt	atc	gac	192
Pro	Gly	Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp	
50						55					60					
gcc	gcc	ctc	ccc	gca	acc	gaa	cac	gcc	tac	caa	acc	acc	cct	cac	gac	240
Ala	Ala	Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp	
65					70					75					80	
ggc	gac	act	ctt	cgc	gtt	gtg	gct	gat	att	ccc	gat	gct	cag	ttc	cgc	288
Gly	Asp	Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg	
				85					90					95		
acc	cag	atc	aat	gag	ctg	aaa	gaa	aac	att	tac	aac	ggt	gac	atc	tac	336
Thr	Gln	Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr	
			100					105					110			
caa	gtt	gtc	ccg	gcg	cgc	act	ttc	acc	gca	cca	tgt	cct	gat	gca	ttc	384
Gln	Val	Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe	
			115				120					125				
gct	gct	tat	ctg	cag	ctg	cgt	gcc	acc	aac	ccg	tcg	ccg	tac	atg	ttc	432
Ala	Ala	Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe	
130						135					140					
tat	atc	cgt	ggc	ctc	aac	gaa	ggc	cgc	tcc	tat	gaa	ctt	ttt	ggc	gca	480
Tyr	Ile	Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala	

145	150	155	160	
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag				528
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln	165	170	175	
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc				576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly	180	185	190	
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act				624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr	195	200	205	
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc				672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg	210	215	220	
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat				720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp	225	230	235	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt				768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg	245	250	255	
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg				816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg	260	265	270	
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct				864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala	275	280	285	
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt				912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly	290	295	300	
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att				960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile	305	310	315	320
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct				1008
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala	325	330	335	
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag				1056
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu	340	345	350	
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct				1104
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala	355	360	365	
ggt tcc act ttg gag gtc atc cga tgacacacgt tgttctcatt gat				1151
Gly Ser Thr Leu Glu Val Ile Arg	370	375		

&lt;210&gt; 422

&lt;211&gt; 376

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 422

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Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
 1             5             10             15

Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
      20             25             30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
      35             40             45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
 50             55             60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
 65             70             75             80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
      85             90             95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
      100             105             110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
 115             120             125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
 130             135             140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
 145             150             155             160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
      165             170             175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
 180             185             190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
 195             200             205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
 210             215             220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
 225             230             235             240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
      245             250             255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg
 260             265             270

Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala
 275             280             285

Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly
 290             295             300

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Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile  
 305 310 315 320

Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala  
 325 330 335

Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu  
 340 345 350

Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala  
 355 360 365

Gly Ser Thr Leu Glu Val Ile Arg  
 370 375

&lt;210&gt; 423

&lt;211&gt; 1068

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1045)

&lt;223&gt; RXA02687

&lt;400&gt; 423

caaaaccatg ctcggcgggg gagagttggg ccaagcgggt cgctaattga gcaacagaca 60

tggacaccca ccttagttcg gcgggttaag ctgtgtaacc atg agc gac gca cca 115  
 Met Ser Asp Ala Pro  
 1 5

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163  
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala  
 10 15 20

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211  
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu  
 25 30 35

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259  
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His  
 40 45 50

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307  
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly  
 55 60 65

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355  
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln  
 70 75 80 85

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403  
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg  
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451  
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val  
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499  
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala  
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547  
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala  
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595  
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu  
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643  
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala  
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691  
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Val Ser Glu Pro  
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739  
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro  
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787  
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp  
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835  
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr  
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883  
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala  
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931  
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val  
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979  
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp  
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc 1027  
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser  
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att 1068  
 Glu Gly Arg Lys Leu Asn  
 310 315

&lt;210&gt; 424

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 424

Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr  
 1 5 10 15

Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly  
                     20                    25                    30  
 Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val  
                     35                    40                    45  
 Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu  
                     50                    55                    60  
 Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln  
                     65                    70                    75                    80  
 Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe  
                     85                    90                    95  
 Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu  
                     100                    105                    110  
 Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr  
                     115                    120                    125  
 Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly  
                     130                    135                    140  
 Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser  
                     145                    150                    155                    160  
 Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala  
                     165                    170                    175  
 Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala  
                     180                    185                    190  
 Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser  
                     195                    200                    205  
 Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala  
                     210                    215                    220  
 Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys  
                     225                    230                    235                    240  
 Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg  
                     245                    250                    255  
 Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu  
                     260                    265                    270  
 Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser  
                     275                    280                    285  
 Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
                     290                    295                    300  
 Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
                     305                    310                    315

&lt;210&gt; 425

&lt;211&gt; 1353

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; RXN01698

&lt;400&gt; 425

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cgctagtgcc tgcagttatg tcgctttttg acgtcgaaaa gcaatttttaa aaagcccttg 60
gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
                                         Met Leu Gly Met Leu
                                         1 5
cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
                        10 15 20
gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
                        25 30 35
tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
                        40 45 50
aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
                        55 60 65
ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
                        70 75 80 85
gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
                        90 95 100
cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
                        105 110 115
cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
                        120 125 130
ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
                        135 140 145
gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
                        150 155 160 165
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
                        170 175 180
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile

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185					190					195						
gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggg	aaa	gac	gct	gaa	gaa	tcc	atg	739
Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	Ala	Glu	Glu	Ser	Met	
		200					205					210				
atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	gat	acc	ctc	ggg	ggc	787
Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	Asp	Thr	Leu	Gly	Gly	
	215					220					225					
atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	ggg	ttg	ggc	tca	cac	835
Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	Gly	Leu	Gly	Ser	His	
	230					235				240					245	
att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	gca	gct	gca	ctc	atg	883
Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	Ala	Ala	Ala	Leu	Met	
				250					255					260		
ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggg	gac	ggg	ttc	gaa	gaa	931
Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	Asp	Gly	Phe	Glu	Glu	
			265					270					275			
gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	gtg	ttc	ctg	gat	gac	979
Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	Val	Phe	Leu	Asp	Asp	
			280				285					290				
aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggg	ggc	ctc	gaa	ggc	ggc	1027
Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	Gly	Leu	Glu	Gly	Gly	
	295					300					305					
atg	acc	aac	ggg	gaa	acc	ctg	cgc	gtt	cgt	gct	ggc	atg	aag	cca	att	1075
Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	Gly	Met	Lys	Pro	Ile	
	310					315				320					325	
tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	atg	gaa	aac	ggc	aag	1123
Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	Met	Glu	Asn	Gly	Lys	
				330					335					340		
gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	tgc	gct	gtt	cca	gcc	1171
Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	Cys	Ala	Val	Pro	Ala	
			345				350						355			
gcc	ggg	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	gtt	ctc	gcc	cgc	gca	1219
Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	Val	Leu	Ala	Arg	Ala	
		360					365					370				
gtc	ctg	cag	aaa	ttc	ggc	ggg	gac	tcc	ctg	agc	gaa	acc	aag	agc	aac	1267
Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser	Glu	Thr	Lys	Ser	Asn	
	375					380					385					
att	gac	acc	tac	ctc	aaa	aac	att	gag	gaa	cga	atg	aaa	ttc	gaa	ggg	1315
Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg	Met	Lys	Phe	Glu	Gly	
	390					395				400					405	
tta	gag	gat	gga	gcg	taatgaagtg	aatgatcaaa	ttc									1353
Leu	Glu	Asp	Gly	Ala												
				410												

&lt;210&gt; 426

&lt;211&gt; 410

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 426

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Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln
 1             5             10             15

Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr
      20             25             30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
      35             40             45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
      50             55             60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
      65             70             75             80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
      85             90             95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
      100            105            110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
      115            120            125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
      130            135            140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
      145            150            155            160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
      165            170            175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
      180            185            190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
      195            200            205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
      210            215            220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
      225            230            235            240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
      245            250            255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
      260            265            270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
      275            280            285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
      290            295            300

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Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320  
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335  
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350  
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

<210> 427  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> FRXA01698

<400> 427  
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 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15  
 ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30  
 ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45  
 atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct 192  
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60  
 tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt 240  
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80  
 tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att 288  
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95  
 tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca 336  
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac	384
Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp	
115 120 125	
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc	432
Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly	
130 135 140	
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc	480
Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile	
145 150 155 160	
ggc ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc	528
Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile	
165 170 175	
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt	576
Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly	
180 185 190	
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa	624
Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu	
195 200 205	
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt	672
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly	
210 215 220	
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct	720
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala	
225 230 235 240	
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat	768
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp	
245 250 255	
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg	816
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val	
260 265 270	
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg	864
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu	
275 280 285	
gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc	912
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser	
290 295 300	
gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga	960
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg	
305 310 315 320	
atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa	1010
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala	
325 330	
ttc	1013

&lt;210&gt; 428

&lt;211&gt; 330



&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 428

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45  
 Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60  
 Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80  
 Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95  
 Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110  
 Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125  
 Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140  
 Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160  
 Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175  
 Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190  
 Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 195 200 205  
 Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 210 215 220  
 Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 225 230 235 240  
 Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 245 250 255  
 Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 260 265 270  
 Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 275 280 285  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

<210> 429

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA01095

<400> 429

gaaaccccag gtcaaagcta ggggtgtggca ccttgatttc tttcgccatg tgtgttcggg 60  
 ataaccttaa acacagcatt gggttgaagg aggttggggc atg gtt gca aca gag 115  
 Met Val Ala Thr Glu  
 1 5  
 aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163  
 Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala  
 10 15 20  
 acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211  
 Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu  
 25 30 35  
 acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259  
 Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn  
 40 45 50  
 gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307  
 Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser  
 55 60 65  
 gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355  
 Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met  
 70 75 80 85  
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403  
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp  
 90 95 100  
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451  
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp  
 105 110 115  
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499  
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile  
 120 125 130  
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547  
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu  
 135 140 145  
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595

Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser  
 150 155 160 165

gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643  
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr  
 170 175 180

gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691  
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro  
 185 190 195

gaa gcg ttt tgc ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739  
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg  
 200 205 210

att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787  
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala  
 215 220 225

cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835  
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr  
 230 235 240 245

aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tgc cgt 883  
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg  
 250 255 260

tgaagagggtg ctctgtggtc agc 906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile  
 1 5 10 15

Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser  
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
 35 40 45

Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
 50 55 60

Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
 65 70 75 80

Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
 85 90 95

Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
 100 105 110

Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
 115 120 125

Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu

130	135	140
Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met		
145	150	155 160
Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val		
	165	170 175
Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly		
	180	185 190
Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro		
	195	200 205
Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu		
	210	215 220
Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His		
	225	230 235 240
Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro		
	245	250 255
Ala Cys Pro Ser Arg		
	260	

<210> 431  
 <211> 1545  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1522)  
 <223> RXA00955

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 aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115  
 Met Thr Ser Asn Asn  
 1 5  
 ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg 163  
 Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu  
 10 15 20  
 gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca 211  
 Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro  
 25 30 35  
 aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg 259  
 Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly  
 40 45 50  
 gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg 307  
 Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met  
 55 60 65  
 att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc 355

Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg		
70					75					80					85		
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc		403
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly		
				90				95						100			
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg		451
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val		
			105					110					115				
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt		499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg		
		120					125					130					
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat		547
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp		
	135					140					145						
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat		595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp		
150					155					160				165			
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag		643
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys		
				170				175						180			
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg		691
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu		
			185					190					195				
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca		739
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala		
		200					205					210					
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc		787
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val		
	215					220					225						
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg		835
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu		
230					235					240				245			
acc	agc	cag	gaa	aac	gtc	gat	ctg	gca	gcc	cgc	gaa	tta	gtc	tac	ggc		883
Thr	Ser	Gln	Glu	Asn	Val	Asp	Leu	Ala	Ala	Arg	Glu	Leu	Val	Tyr	Gly		
				250				255						260			
ccc	aac	aaa	gtc	tgc	gga	ctc	acc	tca	cca	agt	gca	gca	caa	acc	gct		931
Pro	Asn	Lys	Val	Cys	Gly	Leu	Thr	Ser	Pro	Ser	Ala	Ala	Gln	Thr	Ala		
			265				270						275				
cgc	gca	gcg	ggg	ggc	gtc	tac	ggc	ggg	ctc	atc	ttc	gaa	gag	gca	tcg		979
Arg	Ala	Ala	Gly	Ala	Val	Tyr	Gly	Gly	Leu	Ile	Phe	Glu	Glu	Ala	Ser		
		280					285					290					
cca	cgc	aat	gtt	tca	cgt	gaa	aca	ttg	caa	aaa	atc	atc	gcc	gca	gag		1027
Pro	Arg	Asn	Val	Ser	Arg	Glu	Thr	Leu	Gln	Lys	Ile	Ile	Ala	Ala	Glu		
		295				300					305						
ccc	aac	ctg	cgc	tac	gtc	gcg	gtc	agc	cgt	cgc	acc	tcc	ggg	tac	aag		1075
Pro	Asn	Leu	Arg	Tyr	Val	Ala	Val	Ser	Arg	Arg	Thr	Ser	Gly	Tyr	Lys		

310	315	320	325	
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				1123
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				1171
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				1219
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				1267
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys				
	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				1315
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				1363
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				1411
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				1459
Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp				
	440	445	450	
gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc				1507
Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile				
	455	460	465	
tcc aca ttc cat tac taaagggttta aataggatca tga				1545
Ser Thr Phe His Tyr				
470				

&lt;210&gt; 432

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 432

Met	Thr	Ser	Asn	Asn	Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly
1				5					10					15	

Arg	Arg	Gly	His	Leu	Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp
			20					25					30		

Val	Asp	Ala	Leu	Pro	Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn
		35					40					45			

Gln	Gly	Arg	Gly	Gly	Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser
	50					55					60				

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80  
 Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95  
 Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110  
 Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125  
 Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140  
 Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160  
 Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175  
 Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190  
 Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205  
 Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220  
 Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu  
 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly

385		390		395		400
Glu Val Phe Asp Trp	Ala Thr Val Pro	Ala Ala Val Lys	Ala Lys Ser			
	405		410			415
Leu Leu Ala Gly	Gly Ile Ser Pro	Asn Ala Ala Gln	Ala Leu Ala			
	420		425			430
Val Gly Cys Ala Gly	Leu Asp Ile Asn	Ser Gly Val Glu	Tyr Pro Ala			
	435		440			445
Gly Ala Gly Thr Trp	Ala Gly Ala Lys	Asp Ala Gly	Ala Leu Leu Lys			
	450		455			460
Ile Leu Ala Thr Ile	Ser Thr Phe His Tyr					
465		470				

&lt;210&gt; 433

&lt;211&gt; 494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; RXA02814

&lt;400&gt; 433

gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc	48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr	
1 5 10 15	
atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa	96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu	
20 25 30	
ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc	144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly	
35 40 45	
acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca	192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr	
50 55 60	
cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc	240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala	
65 70 75 80	
ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc	288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala	
85 90 95	
ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc	336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg	
100 105 110	
tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc	384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly	
115 120 125	



gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

tcttaaaaca ccg 494

<210> 434

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr  
 1 5 10 15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu  
 20 25 30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly  
 35 40 45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr  
 50 55 60

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80

Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95

Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110

Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125

Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140

Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435

<211> 803

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(780)

<223> RXA00229

<400> 435

gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48  
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile

1	5							10					15					
gac Asp	acg Thr	ctt Leu	ggg Gly 20	tcg Ser	cgt Arg	gct Ala	tcc Ser	ggg Gly 25	caa Gln	gat Asp	tta Leu	aat Asn	acg Thr 30	ctt Leu	ctc Leu	96		
gac Asp	gcc Ala 35	gcc Ala	ctc Leu	tac Tyr	ctt Leu	ggc Gly	ttc Phe 40	agc Ser	ggc Gly	ctg Leu	aac Asn	atc Ile 45	act Thr	cac His	ccg Pro	144		
tac Tyr 50	aag Lys	caa Gln	gca Ala	gta Val	tta Leu	ccc Pro 55	ctg Leu	ctt Leu	ggc Gly	gaa Glu	gtc Val 60	tcc Ser	gaa Glu	caa Gln	gcc Ala	192		
acc Thr 65	caa Gln	ctc Leu	ggc Gly	gca Ala	gtg Val 70	aat Asn	act Thr	gtc Val	gtt Val	atg Met 75	gac Asp	gcc Ala	acc Thr	ggc Gly	cac His 80	240		
acc Thr	acc Thr	ggc Gly	cac His 85	aac Asn	acc Thr	gac Asp	gtc Val	tcc Ser	gga Gly 90	ttt Phe	ggc Gly	cgc Arg	gga Gly 95	atg Met	gaa Glu	288		
gaa Glu	ggc Gly	ctc Leu	ccc Pro 100	aac Asn	gcc Ala	aag Lys	ctc Leu	gat Asp 105	tcc Ser	gtc Val	gtg Val	cag Gln	gtc Val 110	ggc Gly	gcc Ala	336		
ggc Gly	ggc Gly	gta Val 115	gaa Glu	aac Asn	gca Ala	gtg Val	gca Ala	tac Tyr 120	gcc Ala	ctg Leu	gtc Val	acc Thr 125	cac His	ggt Gly	gtg Val	384		
cag Gln 130	aaa Lys	ctt Leu	cag Gln	gtc Val	gct Ala	gac Asp 135	ctc Leu	gac Asp	act Thr	tcc Ser	cgc Arg 140	gcg Ala	cag Gln	gca Ala	ctg Leu	432		
gca Ala 145	gat Asp	gtc Val	atc Ile	aac Asn	aac Asn 150	gca Ala	gtc Val	ggc Gly	cgt Arg	gaa Glu 155	gcc Ala	gtc Val	gtg Val	gga Gly	gta Val 160	480		
gac Asp	gcc Ala	cgc Arg	ggc Gly	atc Ile 165	gaa Glu	gac Asp	gtc Val	atc Ile	gcc Ala 170	gcc Ala	gcc Ala	gac Asp	gga Gly	gta Val 175	gtc Val	528		
aac Asn	gca Ala	acc Thr 180	ccc Pro	atg Met	gga Gly	atg Met	cca Pro	gca Ala 185	cac His	ccc Pro	ggc Gly	acc Thr 190	gcc Ala	ttt Phe	gat Asp	576		
gtc Val	agc Ser	tgc Cys 195	ctc Leu	acc Thr	aag Lys	gat Asp	cac His 200	tgg Trp	gtt Val	ggc Gly	gac Asp	gtc Val 205	gtg Val	tac Tyr	atg Met	624		
ccc Pro	atc Ile 210	gaa Glu	act Thr	gaa Glu	ctt Leu	ctc Leu 215	aaa Lys	gcc Ala	gcc Ala	cgt Arg	gcc Ala 220	ctc Leu	ggc Gly	tgc Cys	gaa Glu	672		
acc Thr 225	ctc Leu	gac Asp	gga Gly	acc Thr	cgc Arg	atg Met 230	gca Ala	atc Ile	cac His	caa Gln 235	gcc Ala	gtc Val	gat Asp	gcc Ala	ttc Phe 240	720		
cga Arg	ctg Leu	ttc Phe	acc Thr 245	ggc Gly	ctc Leu	gaa Glu	ccc Pro	gac Asp	gtc Val 250	tcc Ser	cgc Arg	atg Met	cgg Arg	gaa Glu 255	act Thr	768		

ttc ctg tcc ctc taaaagagtc agtaaacct cga  
 Phe Leu Ser Leu  
 260

803

&lt;210&gt; 436

&lt;211&gt; 260

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15

Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110

Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140

Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160

Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175

Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190

Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205

Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220

Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240

Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255

Phe Leu Ser Leu

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<210> 437
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (904)
<223> RXA02093
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ggcaggaatt tcccgaaaac ttccaccaat aatcaagcca tatcccacac aatcaggcat																60
ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc																115
Met Val Asn Tyr Val																5
gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac																163
Asp Arg Glu Thr 10 Leu Cys Ile Ser 15 Ala Ala Arg Pro Ser Asn 20																
cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac																211
His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn																25 30 35
tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca																259
Tyr Leu Tyr 40 Lys Ala Val Ala Pro 45 Ile Thr 50 Ala Val Ala																
ggt atc cgt ggt ctg aac att cgc ggc gca ggt gtc tcc atg cca tac																307
Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly Val Ser Met Pro Tyr																55 60 65
aag agc gat gtc atc cca ctc atc gat gag ttg cat cct tcc gca gag																355
Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu His Pro Ser Ala Glu																70 75 80 85
cgc ata cgt tct gtt aac acc atc gtc aac aat gac gga cac ctt gtc																403
Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn Asp Gly His Leu Val																90 95 100
gga tac aac acc gac tac act gcg gtg tac cac ctc ctt gaa gaa cac																451
Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His Leu Leu Glu Glu His																105 110 115
cgc gtg aac ccc aat gca cga gta gct atc aag gga tcc ggc ggc atg																499
Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys Gly Ser Gly Gly Met																120 125 130
gcc aat gct gtt gtt gca gct ctt gct gag tat ggt ctg agt ggc acc																547
Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr Gly Leu Ser Gly Thr																135 140 145
gtc gtt gcc cgc aac cac acc acc ggt tct gcg cta gct tcc cgt tac																595
Val Val Ala Arg Asn His Thr Thr Gly Ser Ala Leu Ala Ser Arg Tyr																150 155 160 165
ggt tgg gaa tac tcc gca act gtt ccg gaa gac gca aaa att ttg gtt																643

Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp Ala Lys Ile Leu Val  
 170 175 180  
 aat gta acc cca atg gga atg aat gga cct gac caa gac gtt gta tct 691  
 Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp Gln Asp Val Val Ser  
 185 190 195  
 ttt ggt gag gat gaa gta gac cga gcc gac gta atc ttt gac tgc gta 739  
 Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val Ile Phe Asp Cys Val  
 200 205 210  
 gca ttc ccc gtc gag acc cca ctg att aag ttg gcc aag gaa aag ggt 787  
 Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu Ala Lys Glu Lys Gly  
 215 220 225  
 aag caa acc atc gac ggc gga gaa gtt gcc gct ctt cag gca gca gag 835  
 Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala Leu Gln Ala Ala Glu  
 230 235 240 245  
 cag ttc cac ctc tac acc gga gtt ctt cca acc aac gac cag atc att 883  
 Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr Asn Asp Gln Ile Ile  
 250 255 260  
 gct gcg gag gag ttc tcc aag taaattttctc tcccctattt tta 927  
 Ala Ala Glu Glu Phe Ser Lys  
 265  
 <210> 438  
 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 438  
 Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala  
 1 5 10 15  
 Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala  
 20 25 30  
 Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile  
 35 40 45  
 Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly  
 50 55 60  
 Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu  
 65 70 75 80  
 His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn  
 85 90 95  
 Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His  
 100 105 110  
 Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys  
 115 120 125  
 Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr  
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala  
 145 150 155 160  
 Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp  
 165 170 175  
 Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp  
 180 185 190  
 Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val  
 195 200 205  
 Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu  
 210 215 220  
 Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala  
 225 230 235 240  
 Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr  
 245 250 255  
 Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys  
 260 265

&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttcttag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115  
 Leu Gly Ser His Ile  
 1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163  
 Thr His Arg Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser  
 10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211  
 Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp  
 25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259  
 Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val  
 40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307  
 Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser  
 55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355  
 Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys  
 70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403  
 Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg  
 90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451  
 Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu  
 105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499  
 Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser  
 120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547  
 Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val  
 135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595  
 Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln  
 150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643  
 Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu  
 170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691  
 His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala  
 185 190 195

gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
 265 270 275

taagtccccg ccacctcctc aac 951

&lt;210&gt; 440

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
 1 5 10 15

Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
                   20                                  25                                  30  
 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
                   35                                  40                                  45  
 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
                   50                                  55                                  60  
 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
                   65                                  70                                  75                                  80  
 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
                                   85                                  90                                  95  
 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
                   100                                  105                                  110  
 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
                   115                                  120                                  125  
 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
                   130                                  135                                  140  
 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
                   145                                  150                                  155                                  160  
 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
                                   165                                  170                                  175  
 Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
                   180                                  185                                  190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
                   195                                  200                                  205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
                   210                                  215                                  220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
                   225                                  230                                  235                                  240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
                                   245                                  250                                  255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
                   260                                  265                                  270  
 Ser Glu Glu His  
                   275

&lt;210&gt; 441

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA01699



&lt;400&gt; 441

ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60

aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
Met Glu Arg Asn Glu  
1 5

gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu  
10 15 20

tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys  
25 30 35

tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val  
40 45 50

gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala  
55 60 65

gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile  
70 75 80 85

cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403  
His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
90 95 100

gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp  
105 110 115

gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala  
120 125 130

aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His  
135 140 145

tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala  
150 155 160 165

acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala  
170 175 180

gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
Ala Val Leu His His Leu Glu Ile Asp  
185 190

tta 693

&lt;210&gt; 442

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

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Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
 1           5           10           15

Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
          20           25           30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
          35           40           45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50           55           60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65           70           75           80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
          85           90           95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
          100          105          110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
          115          120          125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala
          130          135          140

Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu
          145          150          155          160

Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro
          165          170          175

Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp
          180          185          190

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&lt;210&gt; 443

&lt;211&gt; 959

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (97)..(936)

&lt;223&gt; RXA00952

&lt;400&gt; 443

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catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60

cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat      114
                      Met Ser Arg Tyr Asp Asp
                      1           5

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc      162
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe
          10           15           20

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atc	atg	ctg	agc	gac	cct	tca	cca	gag	gag	gct	ttc	cag	atc	atc	tcc	210
Ile	Met	Leu	Ser	Asp	Pro	Ser	Pro	Glu	Glu	Ala	Phe	Gln	Ile	Ile	Ser	
		25					30					35				
aca	gca	atc	gaa	gct	ggc	gca	gat	gca	ctg	gaa	ctt	ggc	gta	cct	ttc	258
Thr	Ala	Ile	Glu	Ala	Gly	Ala	Asp	Ala	Leu	Glu	Leu	Gly	Val	Pro	Phe	
	40					45					50					
tcc	gac	cca	gtt	gcc	gat	ggc	ccc	acc	gtc	gcg	gaa	tcc	cac	ctc	cgc	306
Ser	Asp	Pro	Val	Ala	Asp	Gly	Pro	Thr	Val	Ala	Glu	Ser	His	Leu	Arg	
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Ala	Leu	Asp	Gly	Gly	Ala	Thr	Val	Asp	Ser	Ala	Leu	Glu	Gln	Ile	Lys	
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cgc	gtg	cgc	gca	gcc	tac	cca	gag	gtt	ccc	atc	gga	atg	ctc	atc	tac	402
Arg	Val	Arg	Ala	Ala	Tyr	Pro	Glu	Val	Pro	Ile	Gly	Met	Leu	Ile	Tyr	
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Gly	Asn	Val	Pro	Phe	Thr	Arg	Gly	Leu	Asp	Arg	Phe	Tyr	Gln	Glu	Phe	
	105						110					115				
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Ala	Glu	Ala	Gly	Ala	Asp	Ser	Ile	Leu	Leu	Pro	Asp	Val	Pro	Val	Arg	
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gaa	ggc	gca	ccg	ttt	tct	gca	gca	gct	gca	gca	gcc	gga	att	gat	ccc	546
Glu	Gly	Ala	Pro	Phe	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Ile	Asp	Pro	
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att	tac	atc	gct	ccg	gcc	aac	gcc	agc	gag	aaa	acc	ctc	gag	ggt	gtc	594
Ile	Tyr	Ile	Ala	Pro	Ala	Asn	Ala	Ser	Glu	Lys	Thr	Leu	Glu	Gly	Val	
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tcc	gcc	gca	tca	aag	ggc	tac	atc	tac	gcc	atc	tcc	cgc	gac	ggc	gtc	642
Ser	Ala	Ala	Ser	Lys	Gly	Tyr	Ile	Tyr	Ala	Ile	Ser	Arg	Asp	Gly	Val	
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Thr	Gly	Thr	Glu	Arg	Glu	Ser	Ser	Thr	Asp	Gly	Leu	Ser	Ala	Val	Val	
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gac	aac	atc	aag	aaa	ttt	gat	ggc	gca	ccc	atc	ctc	ttg	ggc	ttc	ggc	738
Asp	Asn	Ile	Lys	Lys	Phe	Asp	Gly	Ala	Pro	Ile	Leu	Leu	Gly	Phe	Gly	
	200					205					210					
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Ile	Ser	Ser	Pro	Gln	His	Val	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Ala	Ser	
	215				220				225						230	
ggt	gcg	atc	acg	ggt	tcc	gcg	atc	acc	aag	atc	att	gct	tcc	cac	tgc	834
Gly	Ala	Ile	Thr	Gly	Ser	Ala	Ile	Thr	Lys	Ile	Ile	Ala	Ser	His	Cys	
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gaa	ggt	gag	cac	ccg	aac	ccg	tcc	acc	att	cga	gat	atg	gac	ggt	ttg	882
Glu	Gly	Glu	His	Pro	Asn	Pro	Ser	Thr	Ile	Arg	Asp	Met	Asp	Gly	Leu	
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Lys Val  
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<213> Corynebacterium glutamicum

<400> 444

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Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
35 40 45

Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
50 55 60

Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro  
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp  
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu  
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala  
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Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu  
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala  
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp  
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro  
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala  
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys  
225 230 235 240

Ile Ile Ala Ser His Cys Gly Gly Gly His Pro Ser Pro Ser Thr Ile

245										250					255				
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										Met Thr Glu Lys Glu									
										1 5									
aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc										163									
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly																			
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ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag										211									
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu																			
25 30 35																			
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc										259									
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu																			
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Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu																			
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Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile																			
70 75 80 85																			
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac										403									
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn																			
90 95 100																			
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc										451									
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg																			
105 110 115																			
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc										499									
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu																			
120 125 130																			
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Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys																			
135 140 145																			

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gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His 185 190 195	691
tac ctt ctg ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val 200 205 210	739
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu 215 220 225	787
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly 230 235 240 245	835
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gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp 330 335 340	1123
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atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctg aag cgc Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg 360 365 370	1219
gcc aag acc gcc gaa gta Ala Lys Thr Ala Glu Val 375	1237

&lt;210&gt; 446

&lt;211&gt; 379

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 446

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Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
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Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
      35          40          45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
      50          55          60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
      65          70          75          80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
      85          90          95

Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
      100          105          110

Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
      115          120          125

Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
      130          135          140

Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
      145          150          155          160

Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
      165          170          175

Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
      180          185          190

Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
      195          200          205

Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
      210          215          220

Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
      225          230          235          240

Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
      245          250          255

Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
      260          265          270

Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
      275          280          285

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Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300

Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
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Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr  
 325 330 335

Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala  
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Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala  
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Tyr Ala Leu Lys Arg Ala Lys Thr Ala Glu Val  
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 Met Thr Glu Lys Glu  
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aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
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 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu  
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aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259  
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu  
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307  
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu  
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tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355  
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile  
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ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403  
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn  
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451



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Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Thr	Ala	Thr	Ala	Leu	
		120					125					130				
gca	tgt	gcg	ctc	atg	ggc	ctc	gag	tgc	gtt	gtc	tac	atg	ggc	gcc	aag	547
Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val	Tyr	Met	Gly	Ala	Lys	
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gac	gtt	gcc	cgc	cag	cag	ccc	aac	gtc	tac	cgc	atg	cag	ctg	cac	ggc	595
Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg	Met	Gln	Leu	His	Gly	
150					155					160					165	
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Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly	Thr	Leu	Lys	Asp	Ala	
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gtg	aat	gaa	gcg	ctg	cgc	gat	tgg	acc	gca	acc	ttc	cac	gag	tcc	cac	691
Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr	Phe	His	Glu	Ser	His	
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tac	ctt	ctc	ggc	acc	ccc	gcc	ggc	ccg	cac	cca	ttc	cca	acc	atc	gtg	739
Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro	Phe	Pro	Thr	Ile	Val	
		200					205					210				
cgt	gaa	ttc	cac	aag	gtg	atc	tct	gag	gaa	gcc	aag	gca	cag	atg	cta	787
Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala	Lys	Ala	Gln	Met	Leu	
	215					220					225					
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Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val	Ala	Cys	Val	Gly	Gly	
230					235					240				245		
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Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe	Ile	Asp	Asp	Glu	Gly	
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Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu	Gly	Leu	Asp	Ser	Gly	
			265					270					275			
aag	cac	ggc	gca	acc	atc	acc	aac	ggg	cag	atc	ggc	atc	ctg	cac	ggc	979
Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile	Gly	Ile	Leu	His	Gly	
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acc	cgt	tcc	tac	ctg	atg	cgc	aac	tcc	gac	ggc	caa	gtg	gaa	gag	tcc	1027
Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly	Gln	Val	Glu	Glu	Ser	
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tac	tcc	atc	tcc	gcc	gga	ctt	gat	tac	cca	ggc	gtc	ggc	cca	cag	cac	1075
Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	Val	Gly	Pro	Gln	His	
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gca	cac	ctg	cac	gcc	acc	ggc	cgc	gcc	acc	tac	gtt	ggt	atc	acc	gac	1123
Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr	Val	Gly	Ile	Thr	Asp	
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gcc	gaa	gcc	ctc	caa	gca	ttc	cag	tac	ctc	gcc	cgc	tac	gaa	ggc	atc	1171
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	20		25		30	
Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu						
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Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro						
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Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys						
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Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly						
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Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg						
	100		105		110	
Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly						
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Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val						
	130		135		140	
Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg						
	145		150		155	160
Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly						
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Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr						
	180		185		190	
Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro						
	195		200		205	
Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala						
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Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val						
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Met Ser Ser Val Ser																
1 5																
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Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile																
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Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu																
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act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg																259
Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu																
40 45 50																
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Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp																
55 60 65																

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Trp	Ala	Asp	Leu	Leu	Gly	Val	Pro	Val	Glu	Gln	Val	Leu	Ala	Gly	Asp	
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gct	tcg	agc	ttg	aac	atc	atg	ttt	gat	gtg	atc	agc	tgg	tcg	tac	att	451
Ala	Ser	Ser	Leu	Asn	Ile	Met	Phe	Asp	Val	Ile	Ser	Trp	Ser	Tyr	Ile	
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ttc	ggt	aac	aat	gat	tcg	gtt	cag	cct	tgg	tcg	aag	gaa	gaa	acc	gtt	499
Phe	Gly	Asn	Asn	Asp	Ser	Val	Gln	Pro	Trp	Ser	Lys	Glu	Glu	Thr	Val	
		120					125					130				
aag	tgg	att	tgc	cct	gtt	ccg	ggc	tat	gat	cgc	cat	ttc	tcc	atc	acg	547
Lys	Trp	Ile	Cys	Pro	Val	Pro	Gly	Tyr	Asp	Arg	His	Phe	Ser	Ile	Thr	
	135					140					145					
gag	cgt	ttc	ggc	ttt	gag	atg	att	tct	gtg	cca	atg	aat	gaa	gac	ggc	595
Glu	Arg	Phe	Gly	Phe	Glu	Met	Ile	Ser	Val	Pro	Met	Asn	Glu	Asp	Gly	
150					155					160					165	
cct	gat	atg	gat	gct	gtt	gag	gaa	ttg	gtg	aag	aat	ccg	cag	gtt	aag	643
Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys	Asn	Pro	Gln	Val	Lys	
				170					175					180		
ggc	atg	tgg	gtt	gtt	ccg	gtg	ttt	tct	aac	ccg	act	ggt	ttc	acg	gtg	691
Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro	Thr	Gly	Phe	Thr	Val	
			185					190						195		
aca	gaa	gac	gtc	gca	aag	cgt	cta	agc	gca	atg	gaa	acc	gca	gct	ccg	739
Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met	Glu	Thr	Ala	Ala	Pro	
			200				205					210				
gac	ttc	cgc	gtt	gtg	tgg	gat	aat	gcc	tac	gcc	gtt	cat	acg	ctg	acc	787
Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala	Val	His	Thr	Leu	Thr	
	215					220					225					
gat	gaa	ttc	cct	gag	gtt	atc	gat	atc	gtc	ggg	ctt	ggt	gag	gcc	gct	835
Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly	Leu	Gly	Glu	Ala	Ala	
230					235					240					245	
ggc	aac	ccg	aac	cgt	ttc	tgg	gcg	ttc	act	tct	act	tcg	aag	atc	act	883
Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser	Thr	Ser	Lys	Ile	Thr	
				250					255					260		
ctc	gcg	ggt	gcg	ggc	gtg	tcg	ttc	ttc	ctc	acc	tct	gcg	gag	aac	cgc	931
Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr	Ser	Ala	Glu	Asn	Arg	
			265					270					275			
aag	tgg	tac	acc	ggc	cat	gcg	ggt	atc	cgt	ggc	att	ggc	cct	aac	aag	979
Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly	Ile	Gly	Pro	Asn	Lys	
		280					285					290				
gtc	aat	cag	ttg	gct	cat	gcg	cgt	tac	ttt	ggc	gat	gct	gag	gga	gtg	1027
Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly	Asp	Ala	Glu	Gly	Val	
	295					300					305					

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac 1075  
 Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn  
 310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg 1123  
 Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala  
 330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt 1171  
 Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val  
 345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
 410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca 1401  
 Glu His Tyr Ala Asn  
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<210> 450  
 <211> 426  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 450  
 Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu  
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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser

115					120					125						
Lys	Glu	Glu	Thr	Val	Lys	Trp	Ile	Cys	Pro	Val	Pro	Gly	Tyr	Asp	Arg	
130					135					140						
His	Phe	Ser	Ile	Thr	Glu	Arg	Phe	Gly	Phe	Glu	Met	Ile	Ser	Val	Pro	
145					150					155					160	
Met	Asn	Glu	Asp	Gly	Pro	Asp	Met	Asp	Ala	Val	Glu	Glu	Leu	Val	Lys	
165					170					175						
Asn	Pro	Gln	Val	Lys	Gly	Met	Trp	Val	Val	Pro	Val	Phe	Ser	Asn	Pro	
180					185					190						
Thr	Gly	Phe	Thr	Val	Thr	Glu	Asp	Val	Ala	Lys	Arg	Leu	Ser	Ala	Met	
195					200					205						
Glu	Thr	Ala	Ala	Pro	Asp	Phe	Arg	Val	Val	Trp	Asp	Asn	Ala	Tyr	Ala	
210					215					220						
Val	His	Thr	Leu	Thr	Asp	Glu	Phe	Pro	Glu	Val	Ile	Asp	Ile	Val	Gly	
225					230					235					240	
Leu	Gly	Glu	Ala	Ala	Gly	Asn	Pro	Asn	Arg	Phe	Trp	Ala	Phe	Thr	Ser	
245					250					255						
Thr	Ser	Lys	Ile	Thr	Leu	Ala	Gly	Ala	Gly	Val	Ser	Phe	Phe	Leu	Thr	
260					265					270						
Ser	Ala	Glu	Asn	Arg	Lys	Trp	Tyr	Thr	Gly	His	Ala	Gly	Ile	Arg	Gly	
275					280					285						
Ile	Gly	Pro	Asn	Lys	Val	Asn	Gln	Leu	Ala	His	Ala	Arg	Tyr	Phe	Gly	
290					295					300						
Asp	Ala	Glu	Gly	Val	Arg	Ala	Val	Met	Arg	Lys	His	Ala	Ala	Ser	Leu	
305					310					315					320	
Ala	Pro	Lys	Phe	Asn	Lys	Val	Leu	Glu	Ile	Leu	Asp	Ser	Arg	Leu	Ala	
325					330					335						
Glu	Tyr	Gly	Val	Ala	Gln	Trp	Thr	Val	Pro	Ala	Gly	Gly	Tyr	Phe	Ile	
340					345					350						
Ser	Leu	Asp	Val	Val	Pro	Gly	Thr	Ala	Ser	Arg	Val	Ala	Glu	Leu	Ala	
355					360					365						
Lys	Glu	Ala	Gly	Ile	Ala	Leu	Thr	Gly	Ala	Gly	Ser	Ser	Tyr	Pro	Leu	
370					375					380						
Arg	Gln	Asp	Pro	Glu	Asn	Lys	Asn	Leu	Arg	Leu	Ala	Pro	Ser	Leu	Pro	
385					390					395					400	
Pro	Val	Glu	Glu	Leu	Glu	Val	Ala	Met	Asp	Gly	Val	Ala	Thr	Cys	Val	
405					410					415						
Leu	Leu	Ala	Ala	Ala	Glu	His	Tyr	Ala	Asn							
420					425											

&lt;210&gt; 451

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<220>  
<221> CDS  
<222> (101) .. (1120)  
<223> RXN00448
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gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691

Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser		
			185					190					195				
cat	tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	739	
His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn		
		200					205					210					
ggt	ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	787	
Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser		
	215					220					225						
acc	cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	835	
Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu		
230					235					240					245		
agc	aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	883	
Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile		
				250					255						260		
ctc	cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	931	
Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu		
			265					270						275			
caa	ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	979	
Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg		
		280					285					290					
tcc	ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	1027	
Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser		
	295					300					305						
tcc	agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tggt	gag	aag	1075	
Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys		
310					315					320					325		
cag	ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc		1120	
Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
				330					335					340			
tagttttatc	ggctgatgat	tct														1143	

&lt;210&gt; 452

&lt;211&gt; 340

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 452

Val	Thr	Thr	Lys	Asp	Ile	Ser	Arg	Pro	Val	Cys	Ile	Leu	Gly	Leu	Gly		
1				5					10					15			
Leu	Ile	Gly	Gly	Ser	Leu	Leu	Arg	Asp	Leu	His	Ala	Ala	Asn	His	Ser		
			20					25					30				
Val	Phe	Gly	Tyr	Asn	Arg	Ser	Arg	Ser	Gly	Ala	Lys	Ser	Ala	Val	Asp		
		35					40					45					
Glu	Gly	Phe	Asp	Val	Ser	Ala	Asp	Leu	Glu	Ala	Thr	Leu	Gln	Arg	Ala		
	50					55					60						
Ala	Ala	Glu	Asp	Ala	Leu	Ile	Val	Leu	Ala	Val	Pro	Met	Thr	Ala	Ile		



65					70					75					80
Asp	Ser	Leu	Leu	Asp	Ala	Val	His	Thr	His	Ala	Pro	Asn	Asn	Gly	Phe
				85					90					95	
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
		100						105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
	130					135					140				
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
145					150					155					160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
				165					170					175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
		195					200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
	210					215					220				
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
225					230					235					240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
				245					250					255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
			260					265					270		
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
		275					280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
	290					295					300				
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
305					310					315					320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
				325					330					335	
Ile	Glu	Val	Phe												
			340												

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

<223> FRXA00448

tat	gtg	gga	tcc	cac	ccc	atg	gca	ggc	acc	gcc	aac	tcc	ggc	tgg	agc	48
Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20					25					30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
65				70					75						80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggc	gac	aac	ggc	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
				85					90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100				105						110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
145				150					155						160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
				165				170						175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180				185						190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	

&lt;210&gt; 454

&lt;211&gt; 222

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser  
 1 5 10 15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe  
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile  
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val  
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser His  
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly  
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr  
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser  
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu  
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln  
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser  
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser  
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln  
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 210 215 220

&lt;210&gt; 455

&lt;211&gt; 346

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(346)

&lt;223&gt; FRXA00452

&lt;400&gt; 455

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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60
catagagata accgtagtag gtatgtgcca cacttgtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                               10                               15                               20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                               25                               30                               35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                               40                               45                               50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                               55                               60                               65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
70                               75                               80

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&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 456

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Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
  1                               5                               10                               15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
                20                25                30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
                35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
  50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
  65                70                75                80

Asp Ser

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&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457

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tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60

agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
                               Met His Ser Pro Glu
                               1           5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
          10                      15                      20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
          25                      30                      35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
          40                      45                      50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
          55                      60                      65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
          70                      75                      80                      85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
          90                      95                      100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
          105                      110                      115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
          120                      125                      130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
          135                      140                      145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
          150                      155                      160                      165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
          170                      175                      180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
          185                      190                      195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
          200                      205                      210

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gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787  
 Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr  
 215 220 225  
 tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245  
 tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260  
 gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275  
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290  
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305  
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325  
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340  
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355  
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca 1219  
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala  
 360 365 370  
 gcc aag taattaaggg cgctagactg tta 1248  
 Ala Lys  
 375

&lt;210&gt; 458

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15  
 Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30  
 Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
 35 40 45  
 Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe

50	55	60
Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val 65 70 75 80		
His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu 85 90 95		
Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe 100 105 110		
Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro 115 120 125		
His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg 130 135 140		
Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu 145 150 155 160		
Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp 165 170 175		
Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu 180 185 190		
Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly 195 200 205		
Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His 210 215 220		
Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr 225 230 235 240		
Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly 245 250 255		
Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly 260 265 270		
Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys 275 280 285		
Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile 290 295 300		
Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu 305 310 315 320		
Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly 325 330 335		
Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp 340 345 350		
Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg 355 360 365		
Glu Arg Arg Ala Ala Ala Lys 370 375		

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<220>  
<221> CDS  
<222> (101) .. (1960)  
<223> RXA00579
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<400> 459																	
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gtgcttttct	cgttgttttg	tggttttgtc	agaggatgtc	atg	cgc	ggt	tta	att	115								
				Met	Arg	Val	Leu	Ile	5								
				1													
att	gat	aat	tat	gat	tct	ttc	acg	ttt	aat	ctc	gcc	acc	tat	gtg	gaa	163	
Ile	Asp	Asn	Tyr	Asp	Ser	Phe	Thr	Phe	Asn	Leu	Ala	Thr	Tyr	Val	Glu		
				10					15					20			
gag	gtt	acg	ggt	cag	gca	cct	gtg	gtg	gtg	cct	aat	gat	caa	gaa	ata	211	
Glu	Val	Thr	Gly	Gln	Ala	Pro	Val	Val	Val	Pro	Asn	Asp	Gln	Glu	Ile		
				25					30					35			
gat	gag	atg	ctt	ttc	gac	gcc	gtc	atc	ctc	tca	cct	ggc	ccg	ggc	cac	259	
Asp	Glu	Met	Leu	Phe	Asp	Ala	Val	Ile	Leu	Ser	Pro	Gly	Pro	Gly	His		
				40					45					50			
gcc	ggc	gtt	gcg	gct	gat	ttt	ggt	atc	tgt	gca	ggc	gtc	att	gag	cgt	307	
Ala	Gly	Val	Ala	Ala	Asp	Phe	Gly	Ile	Cys	Ala	Gly	Val	Ile	Glu	Arg		
				55					60					65			
gca	cgc	gtt	ccg	att	ttg	ggt	gtg	tgt	tta	ggc	cac	cag	ggc	att	gcg	355	
Ala	Arg	Val	Pro	Ile	Leu	Gly	Val	Cys	Leu	Gly	His	Gln	Gly	Ile	Ala		
				70					75					80			
ttg	gcc	tat	ggc	ggt	gat	gtt	gat	ttg	gcg	ccc	agg	ccg	gtc	cac	ggt	403	
Leu	Ala	Tyr	Gly	Gly	Asp	Val	Asp	Leu	Ala	Pro	Arg	Pro	Val	His	Gly		
				90					95					100			
gag	gtt	tcg	cag	atc	acc	cat	gat	ggt	tca	ggt	tta	ttt	gca	ggc	atc	451	
Glu	Val	Ser	Gln	Ile	Thr	His	Asp	Gly	Ser	Gly	Leu	Phe	Ala	Gly	Ile		
				105					110					115			
cct	gaa	acg	ttt	gag	gcg	gtg	cgt	tat	cac	tcg	atg	gtg	gca	acc	cgc	499	
Pro	Glu	Thr	Phe	Glu	Ala	Val	Arg	Tyr	His	Ser	Met	Val	Ala	Thr	Arg		
				120					125					130			
ttg	ccg	gag	tca	ttg	aaa	gct	aca	gct	acc	agc	gat	gat	ggt	ttg	atc	547	
Leu	Pro	Glu	Ser	Leu	Lys	Ala	Thr	Ala	Thr	Ser	Asp	Asp	Gly	Leu	Ile		
				135					140					145			
atg	gca	ttg	gca	cat	gaa	gtg	ctt	ccg	cag	tgg	ggt	gtg	caa	ttt	cat	595	
Met	Ala	Leu	Ala	His	Glu	Val	Leu	Pro	Gln	Trp	Gly	Val	Gln	Phe	His		
				150					155					160			
ccg	gaa	tct	att	ggt	gga	caa	ttc	ggc	cat	cag	atc	att	aag	aac	ttc	643	
Pro	Glu	Ser	Ile	Gly	Gly	Gln	Phe	Gly	His	Gln	Ile	Ile	Lys	Asn	Phe		



170										175										180									
ctt	aat	tta	gcg	cgc	aca	tat	cgc	tgg	caa	ctc	acg	gag	aaa	act	att	691													
Leu	Asn	Leu	Ala	Arg	Thr	Tyr	Arg	Trp	Gln	Leu	Thr	Glu	Lys	Thr	Ile														
			185				190						195																
ccg	ctc	agc	ggt	gat	tca	gca	gcg	ggt	ttt	gaa	aca	ttc	ttt	gcc	cat	739													
Pro	Leu	Ser	Val	Asp	Ser	Ala	Ala	Val	Phe	Glu	Thr	Phe	Phe	Ala	His														
			200				205						210																
tcc	tcc	cat	gct	ttt	tgg	ctc	gat	gat	gcc	caa	gga	acc	agc	tat	ctt	787													
Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln	Gly	Thr	Ser	Tyr	Leu														
			215				220						225																
ggt	gat	gcc	agc	ggt	cct	ctc	gca	cgc	aca	aaa	acc	cat	aat	gtc	ggc	835													
Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys	Thr	His	Asn	Val	Gly														
			230				235						240			245													
gag	ggg	gat	ttc	ttc	acc	tgg	cta	aag	gag	gat	ctc	gcc	gcc	aac	tca	883													
Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp	Leu	Ala	Ala	Asn	Ser														
			250				255						260																
ggt	gcg	ccc	ggt	caa	ggt	ttt	cgt	ctt	ggc	tgg	ggt	ggt	tac	gtt	ggt	931													
Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp	Val	Gly	Tyr	Val	Gly														
			265				270						275																
tat	gag	ctt	aaa	gcg	gaa	gct	ggc	gca	cgg	gct	gcg	cac	act	tcg	agt	979													
Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala	Ala	His	Thr	Ser	Ser														
			280				285						290																
ctt	ccg	gat	gcg	cac	ctc	att	ttt	gcc	gat	cgc	gcc	atc	gca	gtg	gaa	1027													
Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg	Ala	Ile	Ala	Val	Glu														
			295				300						305																
tcg	gat	cag	ggt	cgg	ttg	ctg	gcg	ttg	ggg	gag	cag	gac	gag	tgg	ttt	1075													
Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu	Gln	Asp	Glu	Trp	Phe														
			310				315						320			325													
gaa	gaa	acc	atc	aag	aag	ctg	cat	aat	ctt	gtc	gcc	ccg	cgg	ata	cct	1123													
Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val	Ala	Pro	Arg	Ile	Pro														
			330				335						340																
gcg	tcc	gga	cac	ctc	gct	ttg	cag	ggt	cga	gat	tcc	aaa	gat	gag	tat	1171													
Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp	Ser	Lys	Asp	Glu	Tyr														
			345				350						355																
ctc	gac	aaa	att	cgc	aga	gcc	cag	gag	ctg	att	act	cgc	ggc	gaa	tcg	1219													
Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile	Thr	Arg	Gly	Glu	Ser														
			360				365						370																
tat	gaa	atc	tgc	ctg	acc	aca	aaa	ctt	cag	ggc	acc	act	gat	gtg	gcc	1267													
Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly	Thr	Thr	Asp	Val	Ala														
			375				380						385																
cct	ctg	gct	gcc	tat	cta	gca	ctg	cgt	ggg	gcc	aat	ccc	acc	gca	tat	1315													
Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala	Asn	Pro	Thr	Ala	Tyr														
			390				395						400			405													
ggt	gcg	tat	ctt	cag	ctg	ggg	gat	acc	tct	att	ttg	agt	tcc	tcg	ccg	1363													
Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile	Leu	Ser	Ser	Ser	Pro														
			410				415						420																

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555  
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747  
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
 535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795  
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
 550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843  
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
 570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg 1891  
 His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
 585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat 1939  
 Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
 600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt 1983  
 Leu Phe Gly Val Glu Phe Pro  
 615 620

&lt;210&gt; 460

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu

1	5	10	15
Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro	20	25	30
Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser	35	40	45
Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala	50	55	60
Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly	65	70	75
His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro	85	90	95
Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly	100	105	110
Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser	115	120	125
Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser	130	135	140
Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp	145	150	155
Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln	165	170	175
Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu	180	185	190
Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu	195	200	205
Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln	210	215	220
Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys	225	230	235
Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp	245	250	255
Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp	260	265	270
Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala	275	280	285
Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg	290	295	300
Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu	305	310	315
Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val	325	330	335

Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp  
 450 455 460  
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala  
 465 470 475 480  
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val  
 485 490 495  
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu  
 500 505 510  
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly  
 515 520 525  
 Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540  
 Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560  
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575  
 Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590  
 Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605  
 Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

&lt;210&gt; 461

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXA00958

&lt;400&gt; 461

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ccattgcgct tgctgctggg tccactttgg aggtcatccg atg aca cac gtt gtt 115
                                         Met Thr His Val Val
                                         1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
                        10                        15                        20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
                        25                        30                        35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
                        40                        45                        50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
                        55                        60                        65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
                        70                        75                        80                        85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                        90                        95                        100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                        105                        110                        115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
                        120                        125                        130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
                        135                        140                        145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
                        150                        155                        160                        165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                        170                        175                        180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                        185                        190                        195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744

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Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205

tca

747

<210> 462

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
 130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr  
 145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp  
 165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro  
 180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 195 200 205

<210> 463

<211> 469

<212> DNA

<213> Corynebacterium glutamicum

<220>

<400> 463

<400> 464

Met	Thr	Ser	Pro	Ala	Thr	Leu	Lys	Val	Leu	Asn	Ala	Tyr	Leu	Asp	Asn
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Pro	Thr	Pro	Thr	Leu	Glu	Glu	Ala	Ile	Glu	Val	Phe	Thr	Pro	Leu	Thr
			20					25					30		
Val	Gly	Glu	Tyr	Asp	Asp	Val	His	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Ile
		35					40					45			
Arg	Thr	Arg	Gly	Glu	Gln	Phe	Ala	Asp	Ile	Ala	Gly	Ala	Ala	Lys	Ala
	50					55					60				

Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
 65 70 75 80

Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
 85 90 95

Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
 100 105 110

His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
 115 120

&lt;210&gt; 465

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(541)

&lt;223&gt; RXN02918

&lt;400&gt; 465

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tgattctatt attgccaaat cagaaagcag gagagaccgc atg agc gaa atc cta 115  
 Met Ser Glu Ile Leu  
 1 5

gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
 Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
 10 15 20

ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
 Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His  
 25 30 35

acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc 259  
 Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr  
 40 45 50

gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg 307  
 Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala  
 55 60 65

cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg 355  
 Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu  
 70 75 80 85

ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc 403  
 Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser  
 90 95 100

aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc 451  
 Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser  
 105 110 115

cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct 499  
 Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser



120 125 130  
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac 541  
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp  
135 140 145

taattgtctc ccattttaagg agt 564

<210> 466  
<211> 147  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 466  
Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr  
1 5 10 15  
Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp  
20 25 30  
Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu  
35 40 45  
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe  
50 55 60  
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr  
65 70 75 80  
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg  
85 90 95  
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys  
100 105 110  
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp  
115 120 125  
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly  
130 135 140  
Gln Leu Asp  
145

<210> 467  
<211> 735  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(712)  
<223> RXN01116

<400> 467  
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acaggacggt gtctaactaa tgacttgga tcataaccaa atg gca gcc cgc gtt 115  
Met Ala Ala Arg Val

	1	5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg			163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
	10	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt			211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
	25	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag			259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
	40	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt			307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
	55	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc			355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
	70	80	85
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc			403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
	90	95	100
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag			451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
	105	110	115
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc			499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
	120	125	130
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag			547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
	135	140	145
gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc			595
Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val			
	150	155	160
acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc			643
Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu			
	170	175	180
atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc			691
Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr			
	185	190	195
gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag			735
Glu Ala Asp Phe Lys Val Ala			
	200		

&lt;210&gt; 468

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn  
 1 5 10 15  
 Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30  
 Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45  
 Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60  
 Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80  
 Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95  
 Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110  
 Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125  
 Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140  
 Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160  
 Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175  
 Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190  
 Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala  
 195 200

&lt;210&gt; 469

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXN01115

&lt;400&gt; 469

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gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115  
 Met Ala Ile Leu His  
 1 5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163  
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
 10 15 20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat	211
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His	
25 30 35	
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct	259
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser	
40 45 50	
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg	307
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val	
55 60 65	
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga	355
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly	
70 75 80 85	
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat	403
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp	
90 95 100	
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag	451
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu	
105 110 115	
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act	499
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr	
120 125 130	
ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg	547
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp	
135 140 145	
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc	595
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala	
150 155 160 165	
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc	643
Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr	
170 175 180	
tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc	691
Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr	
185 190 195	
atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc	739
Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile	
200 205 210	
att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca	787
Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro	
215 220 225	
gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg	835
Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu	
230 235 240 245	
cta gca cag cat ttc gct taatgttgta ggcatgttca caa	876
Leu Ala Gln His Phe Ala	
250	

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu  
 1 5 10 15

Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln  
 20 25 30

Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg  
 35 40 45

Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp  
 50 55 60

Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn  
 65 70 75 80

Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu  
 85 90 95

Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala  
 100 105 110

Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys  
 115 120 125

Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp  
 130 135 140

Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe  
 145 150 155 160

Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys  
 165 170 175

Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr  
 180 185 190

Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro  
 195 200 205

Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala  
 210 215 220

Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn  
 225 230 235 240

Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala  
 245 250

&lt;210&gt; 471

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXS00116

&lt;400&gt; 471

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cgcggcacgc acgctggggg caagcgctcga caagcacaaa ctttttgctt aattgaatcc 60
tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
                                         Met Ser Asn Asp Phe
                                         1           5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
                        10                        15                        20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
                        25                        30                        35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
                        40                        45                        50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
                        55                        60                        65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
                        70                        75                        80                        85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                        90                        95                        100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
                        105                        110                        115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
                        120                        125                        130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
                        135                        140                        145

gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
                        150                        155                        160                        165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
                        170                        175                        180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
                        185                        190                        195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln

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200	205	210	
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val 215 220 225			787
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr 230 235 240 245			835
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala 250 255 260			883
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val 265 270 275			931
gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys 280 285 290			979
ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala 295 300 305			1027
ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp 310 315 320 325			1075
att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys 330 335 340			1123
gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys 345 350 355			1171
aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr 360 365 370			1219
ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu 375 380 385			1261
tagtttgaac aggttggttg ggg			1284

&lt;210&gt; 472

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 472

Met	Ser	Asn	Asp	Phe	Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr
1				5					10					15	

Ile	Phe	Ala	Thr	Met	Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn
		20					25					30			

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
                   35                                  40                                  45  
 Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
           50                                  55                                  60  
 Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
       65                                  70                                  75                                  80  
 Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                                  90                                  95  
 Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
                  100                                 105                                 110  
 Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
          115                                 120                                 125  
 Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
       130                                 135                                 140  
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
   145                                 150                                 155                                 160  
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
                  165                                 170                                 175  
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
                  180                                 185                                 190  
 Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
       195                                 200                                 205  
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
       210                                 215                                 220  
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
   225                                 230                                 235                                 240  
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
                  245                                 250                                 255  
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
                  260                                 265                                 270  
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
       275                                 280                                 285  
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
       290                                 295                                 300  
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
   305                                 310                                 315                                 320  
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
                  325                                 330                                 335  
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
       340                                 345                                 350  
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys



[illegible]

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
 150 155 160 165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
 1 5 10 15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
 65 70 75 80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val  
 85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu  
 100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser  
 115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr  
 130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe  
 145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala  
 165

<210> 475

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXS00391

<400> 475

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Leu Leu Arg Asp Ser																
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala																
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu																
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu																
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln																
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp																
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu																
ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag																451
Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln																
tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt																499
Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu																
ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga																547
Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg																
att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc																595
Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser																
tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc																643
Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly																
gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg																691
Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met																
att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac																739
Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn																
gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att																787
Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile																

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc

843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala  
 85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser  
 100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile  
 115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu  
 130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val  
 145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly  
 165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu  
 180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His  
 195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu  
 210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 225 230 235 240

<400> 477  
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gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala

170										175					180					
gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691				
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn					
			185				190						195							
aat	att	cgc	gat	att	cca	acc	gat	agc	aag	acc	gga	aaa	att	acc	ctc	739				
Asn	Ile	Arg	Asp	Ile	Pro	Thr	Asp	Ser	Lys	Thr	Gly	Lys	Ile	Thr	Leu					
			200				205						210							
gcg	gtc	cgc	ctg	ggc	gat	gcg	ggg	gct	cgt	aag	ctg	ttc	ctc	gcg	ctg	787				
Ala	Val	Arg	Leu	Gly	Asp	Ala	Gly	Ala	Arg	Lys	Leu	Phe	Leu	Ala	Leu					
			215				220						225							
att	tcc	acg	cgc	ttc	atc	atg	tcc	atc	tgc	ctg	gcg	ttt	gtc	gcc	tgg	835				
Ile	Ser	Thr	Pro	Phe	Ile	Met	Ser	Ile	Cys	Leu	Ala	Phe	Val	Ala	Trp					
230				235						240			245							
cca	gcg	ctg	atc	gcg	atc	atc	gtt	ttc	ccg	ctg	gca	ctg	aaa	gcc	gca	883				
Pro	Ala	Leu	Ile	Ala	Ile	Ile	Val	Phe	Pro	Leu	Ala	Leu	Lys	Ala	Ala					
			250						255			260								
ggg	ccg	atc	cgc	aac	aac	gcc	acc	ggc	aag	gat	ctc	atc	ccc	gtc	atc	931				
Gly	Pro	Ile	Arg	Asn	Asn	Ala	Thr	Gly	Lys	Asp	Leu	Ile	Pro	Val	Ile					
			265						270			275								
ggc	tca	aca	ggg	cgc	gcc	atg	gcg	ttg	tgg	gcc	gtg	ctc	acg	ggc	ctg	979				
Gly	Ser	Thr	Gly	Arg	Ala	Met	Ala	Leu	Trp	Ala	Val	Leu	Thr	Gly	Leu					
			280						285			290								
gca	tta	gcg	ttt	agc	taaaacgctt	ttcgacgctc	ccc									1017				
Ala	Leu	Ala	Phe	Ser																
295																				

&lt;210&gt; 478

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 478

Met	Ser	His	Thr	Glu	Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp		
1				5				10				15					
Ile	Gln	Gly	Ala	Arg	Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val		
			20				25						30				
Ile	Ala	Gly	Ser	Gly	Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp		
			35				40						45				
Lys	Ala	Leu	Leu	Ala	Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val		
			50				55						60				
Asn	Tyr	Ala	Asn	Asp	Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp		
			65				70						75				
Arg	Thr	Gly	Pro	Leu	Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys		
			85						90						95		
Lys	Val	Lys	Ala	Ala	Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala		
			100						105						110		

Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
 260 265 270  
 Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala  
 275 280 285  
 Val Leu Thr Gly Leu Ala Leu Ala Phe Ser  
 290 295

<210> 479  
 <211> 1005  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(982)  
 <223> FRXA00393

<400> 479  
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 aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115  
 Met Ser His Thr Glu  
 1 5  
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20  
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly

25	30	35	
gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala	259		
40	45	50	
ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	307		
55	60	65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	355		
70	75	80	85
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	403		
90	95	100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	451		
105	110	115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	499		
120	125	130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	547		
135	140	145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	595		
150	155	160	165
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	643		
170	175	180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	691		
185	190	195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	739		
200	205	210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	787		
215	220	225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	835		
230	235	240	245
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	883		
250	255	260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser	931		
265	270	275	





Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255

Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
 260 265 270

Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro  
 275 280 285

Cys Ser Arg Ala Trp His  
 290

&lt;210&gt; 481

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (964)

&lt;223&gt; RXS00446

&lt;400&gt; 481

tgctacgaag ttatctagta atgaagtttag tttttcccct ctcccggcag cagttgatgc 60

ggtgacggag gctacttggg gggctaatacg gtaccgggat atg ggt gcg gtt gag 115  
 Met Gly Ala Val Glu  
 1 5

ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163  
 Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val  
 10 15 20

acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca 211  
 Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala  
 25 30 35

acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259  
 Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu  
 40 45 50

gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att 307  
 Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile  
 55 60 65

ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg 355  
 Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala  
 70 75 80 85

atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403  
 Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro  
 90 95 100

tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451  
 Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys  
 105 110 115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499  
 Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe  
 120 125 130

aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547  
 Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His  
 135 140 145

gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595  
 Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala  
 150 155 160 165

ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643  
 Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala  
 170 175 180

atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691  
 Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285

tgc 987

&lt;210&gt; 482

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 482

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val  
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80  
 Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95  
 Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110  
 Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125  
 Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
 130 135 140  
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
 145 150 155 160  
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
 165 170 175  
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
 180 185 190  
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
 195 200 205  
 Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

&lt;210&gt; 483

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 483

atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat 48  
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
 1 5 10 15

ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
                   20                                  25                                  30

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
                   35                                  40                                  45

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
                   50                                  55                                  60

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
                   65                                  70                                  75                                  80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
                                   85                                  90                                  95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
                   100                                  105                                  110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
                   115                                  120                                  125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
                   130                                  135                                  140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
                   145                                  150                                  155                                  160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
                   165                                  170

tagtcttttg cgttttgcgg tgc 545

&lt;210&gt; 484

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
   1                  5                                  10                                  15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
                   20                                  25                                  30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
                   35                                  40                                  45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
                   50                                  55                                  60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
165 170

<210> 485  
<211> 1230  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1207)  
<223> RXS00618

<400> 485  
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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115  
Met Gln Met Leu Asp  
1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
70 75 80 85

ggg gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403

Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	Leu	Asp	His	Gly	Asp	Tyr	
				90					95					100		
gtg	gca	atg	cct	acc	ccg	ggg	tac	ccg	gca	tat	cgc	aat	att	ctg	gaa	451
Val	Ala	Met	Pro	Thr	Pro	Gly	Tyr	Pro	Ala	Tyr	Arg	Asn	Ile	Leu	Glu	
			105					110					115			
tct	ttg	ggg	gcg	aag	gtt	ctg	aac	ctg	cgc	tgt	act	gca	gag	act	cgt	499
Ser	Leu	Gly	Ala	Lys	Val	Leu	Asn	Leu	Arg	Cys	Thr	Ala	Glu	Thr	Arg	
			120				125					130				
ttc	cag	cca	acc	gct	caa	atg	ttg	gag	gaa	ctg	cca	cac	aag	ccg	aag	547
Phe	Gln	Pro	Thr	Ala	Gln	Met	Leu	Glu	Glu	Leu	Pro	His	Lys	Pro	Lys	
			135				140					145				
gct	gtt	att	gtc	acc	agc	cca	gga	aac	cca	acg	ggc	acc	atc	att	gat	595
Ala	Val	Ile	Val	Thr	Ser	Pro	Gly	Asn	Pro	Thr	Gly	Thr	Ile	Ile	Asp	
					155					160					165	
ccg	gaa	gag	cta	gag	cgc	atc	gcc	aag	tgg	tgc	gat	gac	aat	gat	gct	643
Pro	Glu	Glu	Leu	Glu	Arg	Ile	Ala	Lys	Trp	Cys	Asp	Asp	Asn	Asp	Ala	
				170					175					180		
gtt	ctt	atc	tct	gat	gag	gac	tac	cac	ggc	atg	agc	ttt	ggt	cgt	ccg	691
Val	Leu	Ile	Ser	Asp	Glu	Asp	Tyr	His	Gly	Met	Ser	Phe	Gly	Arg	Pro	
			185					190					195			
ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggt	acc	739
Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	Thr	
			200				205					210				
ttg	tcc	aag	tac	ttc	tcc	atg	acg	ggg	tgg	cgc	gtg	ggt	tgg	atc	atc	787
Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	Ile	
			215			220					225					
gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	ctt	835
Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	Leu	
			230			235				240					245	
tcc	ttg	tgt	gct	cct	gcc	atc	ggg	cag	gct	gcg	gga	cgc	gca	gcc	ttc	883
Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	Phe	
				250				255						260		
act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	cgc	931
Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	Arg	
			265				270						275			
gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	ggc	979
Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	Gly	
			280				285					290				
act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	tct	1027
Thr	Phe	Ala	Asp	Pro	Asp	Gly	Gly	Leu	Tyr	Leu	Trp	Val	Asp	Val	Ser	
			295			300					305					
gca	tac	acc	gat	gat	tca	gag	gaa	tgg	gca	ttg	cgt	ttg	ctc	gat	gaa	1075
Ala	Tyr	Thr	Asp	Asp	Ser	Glu	Glu	Trp	Ala	Leu	Arg	Leu	Leu	Asp	Glu	
					315				320						325	
gcg	ggc	gtg	gcc	gtc	gcg	ccg	ggg	gtt	gat	ttt	gat	cct	gag	gaa	ggc	1123
Ala	Gly	Val	Ala	Val	Ala	Pro	Gly	Val	Asp	Phe	Asp	Pro	Glu	Glu	Gly	

	330	335	340	
cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att				1171
His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile				
	345	350	355	
gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac				1217
Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys				
	360	365		
taggttagtt tcg				1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp				
1	5	10	15	
Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala				
	20	25	30	
Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr				
	35	40	45	
Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp				
	50	55	60	
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val				
	65	70	75	80
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu				
	85	90	95	
Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr				
	100	105	110	
Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys				
	115	120	125	
Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu				
	130	135	140	
Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr				
	145	150	155	160
Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys				
	165	170	175	
Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met				
	180	185	190	
Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala				
	195	200	205	
Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg				
	210	215	220	



Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240

Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255

Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270

Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285

Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300

Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320

Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser  
 340 345 350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
 355 360 365

Lys

<210> 487  
 <211> 657  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(634)  
 <223> FRXA00618

<400> 487  
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 caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
 Met Ser Phe Gly Arg  
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163  
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly  
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307

Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
 55 60 65  
 ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355  
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr  
 70 75 80 85  
 cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
 90 95 100  
 ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
 105 110 115  
 tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
 120 125 130  
 gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547  
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
 135 140 145  
 ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165  
 att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175  
 taggttagtt tcg 657

&lt;210&gt; 488

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15  
 Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30  
 Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45  
 Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60  
 Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80  
 His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95  
 Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125  
 Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140  
 Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160  
 Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175  
 Lys Lys

&lt;210&gt; 489

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 489

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 gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115  
 Met Gln Met Leu Asp  
 1 5  
 cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20  
 gct ggc cag cgc tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35  
 gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50  
 gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65  
 gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85  
 ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

&lt;210&gt; 490

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

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Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
  1             5             10             15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
      20             25             30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
      35             40             45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
      50             55             60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
      65             70             75             80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
      85             90             95

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&lt;210&gt; 491

&lt;211&gt; 1221

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1198)

&lt;223&gt; RXS01105

&lt;400&gt; 491

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ttgtcatcaa ctttgccaac gccgaagatc ttccagcgcga cggcgaagca atccgtgcac 60

gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
                Met Thr Lys Ile Thr
                1             5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
                10             15             20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
                25             30             35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
                40             45             50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
                55             60             65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
                70             75             80             85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile

```

																90																	95																	100																
ctg	cag	cag	ctg	ctg	cag	gct	ttt	ggt	gga	cct	gga	cgc	acc	gcg	ttg	451																																																		
Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	Gly	Arg	Thr	Ala	Leu																																																			
			105							110							115																																																	
gga	ttc	caa	ccc	agc	tat	tcc	atg	cac	cca	att	ttg	gct	aaa	ggc	acc	499																																																		
Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	Leu	Ala	Lys	Gly	Thr																																																			
			120							125							130																																																	
cac	act	gaa	ttc	att	gcg	gtg	tcc	cga	ggt	gct	gat	ttc	cgc	atc	gat	547																																																		
His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	Asp	Phe	Arg	Ile	Asp																																																			
			135							140							145																																																	
atg	gat	gtg	gcg	ctg	gaa	gaa	att	cgt	gca	aag	cag	cct	gac	att	gtt	595																																																		
Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Gln	Pro	Asp	Ile	Val																																																			
			150							155							160																																																	
ttt	gtc	acc	acc	ccg	aac	aac	ccg	acc	ggt	gat	gtg	acc	tcg	ctg	gac	643																																																		
Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	Val	Thr	Ser	Leu	Asp																																																			
			170							175							180																																																	
gat	gtt	gag	cgc	atc	atc	aac	gtt	gcc	cca	ggc	atc	gtg	atc	gtg	gat	691																																																		
Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly	Ile	Val	Ile	Val	Asp																																																			
			185							190							195																																																	
gaa	gct	tat	gcg	gaa	ttc	tcc	cca	tca	cct	tca	gca	acc	act	ctt	ctg	739																																																		
Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	Ala	Thr	Thr	Leu	Leu																																																			
			200							205							210																																																	
gag	aag	tac	cca	acc	aag	ctg	gtg	gtg	tcc	cgc	acc	atg	agt	aag	gct	787																																																		
Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	Thr	Met	Ser	Lys	Ala																																																			
			215							220							225																																																	
ttt	gat	ttc	gca	ggt	gga	cgc	ctc	ggc	tac	ttc	gtg	gcc	aac	cca	gcg	835																																																		
Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	Val	Ala	Asn	Pro	Ala																																																			
			230							235							240																																																	
ttt	atc	gac	gcc	gtg	atg	cta	gtc	cgc	ctt	ccg	tat	cat	ctt	tca	gcg	883																																																		
Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	Tyr	His	Leu	Ser	Ala																																																			
			250							255							260																																																	
ctg	agc	caa	gca	gcc	gca	atc	gta	gcg	ctg	cgt	cac	tcc	gct	gac	acg	931																																																		
Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	His	Ser	Ala	Asp	Thr																																																			
			265							270							275																																																	
ctg	gga	acc	gtc	gaa	aag	ctc	tct	gta	gag	cgt	gtt	cgc	gtg	gca	gca	979																																																		
Leu	Gly	Thr	Val	Glu	Lys	Leu	Ser	Val	Glu	Arg	Val	Arg	Val	Ala	Ala																																																			
			280							285							290																																																	
cgc</																																																																		

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca 1171  
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
                   345                                  350                                  355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca 1218  
 Ala Ala Glu Ile Ile Lys Leu Asn Leu  
                   360                                  365

tga 1221

<210> 492

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 492

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg  
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Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu  
                   20                                  25                                  30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp  
                   35                                  40                                  45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
                   50                                  55                                  60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
                   65                                  70                                  75                                  80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
                   85                                  90                                  95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
                   100                                  105                                  110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
                   115                                  120                                  125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
                   130                                  135                                  140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
                   145                                  150                                  155                                  160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
                   165                                  170                                  175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
                   180                                  185                                  190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
                   195                                  200                                  205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
                   210                                  215                                  220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe

225		230		235		240
Val Ala Asn Pro	Ala Phe Ile Asp	Ala Val Met Leu Val	Arg Leu Pro			
	245	250	255			
Tyr His Leu Ser	Ala Leu Ser Gln	Ala Ala Ile Val	Ala Leu Arg			
	260	265	270			
His Ser Ala Asp	Thr Leu Gly Thr	Val Glu Lys Leu	Ser Val Glu Arg			
	275	280	285			
Val Arg Val Ala	Ala Arg Leu Glu	Glu Leu Gly Tyr	Ala Val Val Pro			
	290	295	300			
Ser Glu Ser Asn	Phe Val Phe Phe	Gly Asp Phe Ser	Asp Gln His Ala			
305	310	315	320			
Ala Trp Gln Ala	Phe Leu Asp Arg	Gly Val Leu Ile	Arg Asp Val Gly			
	325	330	335			
Ile Ala Gly His	Leu Arg Thr Thr	Ile Gly Val Pro	Glu Glu Asn Asp			
	340	345	350			
Ala Phe Leu Asp	Ala Ala Ala Glu	Ile Ile Lys Leu	Asn Leu			
	355	360	365			

<210> 493  
 <211> 1752  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1729)  
 <223> RXS02315

<400> 493  
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 Met Ser Ser Thr Pro  
 1 5  
 gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163  
 Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val  
 10 15 20  
 act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211  
 Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu  
 25 30 35  
 gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259  
 Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu  
 40 45 50  
 cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307  
 Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg  
 55 60 65  
 ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355

Pro	Val	Ala	Val	Val	Met	Thr	Ser	Gly	Thr	Ala	Val	Ala	Asn	Cys	Leu	
70					75					80					85	
cct	gct	gtt	gct	gaa	gct	gcg	cat	gcc	cat	atc	ccg	ttg	att	gtg	ctc	403
Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile	Pro	Leu	Ile	Val	Leu	
				90					95					100		
tct	gct	gac	cgt	cct	gca	cat	ttg	gtg	gga	acg	ggg	gcg	agc	caa	acg	451
Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr	Gly	Ala	Ser	Gln	Thr	
			105					110						115		
att	aac	cag	acc	ggg	att	ttt	ggg	gat	ctt	gca	ccg	acg	gtc	ggg	atc	499
Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala	Pro	Thr	Val	Gly	Ile	
		120					125						130			
act	gag	ctg	gat	cag	gta	gcg	cag	att	gct	gaa	agc	ctt	gct	cag	ggg	547
Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly	
	135					140					145					
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu	
150					155					160					165	
gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	
				170					175					180		
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	
			185					190					195			
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly	
		200					205					210				
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr	
	215					220					225					
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val	
230					235					240					245	
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val	
				250					255					260		
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp	
			265					270					275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp	
		280					285					290				
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc	1027
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly	
	295					300					305					
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt	1075
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu	



310	315	320	325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc				1123
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe				
	330	335	340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc				1171
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly				
	345	350	355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg				1219
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu				
	360	365	370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc				1267
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val				
	375	380	385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct				1315
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala				
	390	395	400	405
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc				1363
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala				
	410	415	420	
ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc				1411
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile				
	425	430	435	
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac				1459
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn				
	440	445	450	
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt				1507
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly				
	455	460	465	
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc				1555
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser				
	470	475	480	485
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac				1603
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp				
	490	495	500	
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc				1651
Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser				
	505	510	515	
gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca				1699
Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala				
	520	525	530	
caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt				1749
Gln Gln Gln Ala Leu Met Asp Thr Val His				
	535	540		
gcg				1752

&lt;210&gt; 494

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 494

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Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
  1             5             10             15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
             20             25             30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
             35             40             45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
             50             55             60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
             65             70             75             80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
             85             90             95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
             100            105            110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
             115            120            125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
             130            135            140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
             145            150            155            160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
             165            170            175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
             180            185            190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
             195            200            205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
             210            215            220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
             225            230            235            240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
             245            250            255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
             260            265            270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
             275            280            285

Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr

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290	295	300
Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser		
305	310	315 320
Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn		
	325	330 335
Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp		
	340	345 350
Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile		
	355	360 365
Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe		
	370	375 380
Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile		
	385	390 395 400
Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala		
	405	410 415
Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile		
	420	425 430
Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr		
	435	440 445
Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu		
	450	455 460
Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr		
	465	470 475 480
Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu		
	485	490 495
His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp		
	500	505 510
Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg		
	515	520 525
Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His		
	530	535 540

&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

gatcttaggc agccgtggga ttacaccctt ttagagctag aacagtaaaa attcacccaa 60

tagctttcaa	ctacgcacac	aaagtggcaa	cattgagcgg	gtg	act	aca	gac	aag	115
				Val	Thr	Thr	Asp	Lys	
				1				5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163								
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala									
	10	15	20						
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat	211								
Asp Gln Ala Ala Arg Pro Thr Arg Thr Thr Arg Arg Ile Phe Asp									
	25	30	35						
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259								
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val									
	40	45	50						
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307								
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys									
	55	60	65						
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355								
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val									
	70	75	80	85					
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403								
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser									
	90	95	100						
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451								
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr									
	105	110	115						
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499								
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu									
	120	125	130						
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547								
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu									
	135	140	145						
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595								
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp									
	150	155	160	165					
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643								
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys									
	170	175	180						
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691								
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys									
	185	190	195						
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739								
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro									
	200	205	210						
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787								
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile									
	215	220	225						
gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc	835								

Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg  
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc 1027  
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc 1267  
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu  
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag 1411  
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435

tagtagttgt taggattcac cac 1434

&lt;210&gt; 496

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn

1	5	10	15
Lys Ala Val Gly	Ala Asp Gln Ala	Ala Arg Pro Thr	Arg Arg Thr Thr
20	25	30	
Arg Arg Ile Phe	Asp Gln Ser Glu	Lys Met Lys Asp	Val Leu Tyr Glu
35	40	45	
Ile Arg Gly Pro	Val Ala Ala Glu	Ala Glu Arg Met	Glu Leu Asp Gly
50	55	60	
His Asn Ile Leu	Lys Leu Asn Thr	Gly Asn Pro Ala	Val Phe Gly Phe
65	70	75	80
Asp Ala Pro Asp	Val Ile Met Arg	Asp Met Ile Ala	Asn Leu Pro Thr
85	90	95	
Ser Gln Gly Tyr	Ser Thr Ser Lys	Gly Ile Ile Pro	Ala Arg Arg Ala
100	105	110	
Val Val Thr Arg	Tyr Glu Val Val	Pro Gly Phe Pro	His Phe Asp Val
115	120	125	
Asp Asp Val Phe	Leu Gly Asn Gly	Val Ser Glu Leu	Ile Thr Met Thr
130	135	140	
Thr Gln Ala Leu	Leu Asn Asp Gly	Asp Glu Val Leu	Ile Pro Ala Pro
145	150	155	160
Asp Tyr Pro Leu	Trp Thr Ala Ala	Thr Ser Leu Ala	Gly Gly Lys Pro
165	170	175	
Val His Tyr Leu	Cys Asp Glu Glu	Asp Asp Trp Asn	Pro Ser Ile Glu
180	185	190	
Asp Ile Lys Ser	Lys Ile Ser Glu	Lys Thr Lys Ala	Ile Val Val Ile
195	200	205	
Asn Pro Asn Asn	Pro Thr Gly Ala	Val Tyr Pro Arg	Arg Val Leu Glu
210	215	220	
Gln Ile Val Glu	Ile Ala Arg Glu	His Asp Leu Leu	Ile Leu Ala Asp
225	230	235	240
Glu Ile Tyr Asp	Arg Ile Leu Tyr	Asp Asp Ala Glu	His Ile Ser Leu
245	250	255	
Ala Thr Leu Ala	Pro Asp Leu Leu	Cys Ile Thr Tyr	Asn Gly Leu Ser
260	265	270	
Lys Ala Tyr Arg	Val Ala Gly Tyr	Arg Ala Gly Trp	Met Val Leu Thr
275	280	285	
Gly Pro Lys Gln	Tyr Ala Arg Gly	Phe Ile Glu Gly	Leu Glu Leu Leu
290	295	300	
Ala Gly Thr Arg	Leu Cys Pro Asn	Val Pro Ala Gln	His Ala Ile Gln
305	310	315	320
Val Ala Leu Gly	Gly Arg Gln Ser	Ile Tyr Asp Leu	Thr Gly Glu His
325	330	335	

Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
                   340                                  345                                  350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
                   355                                  360                                  365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
                   370                                  375                                  380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
                   385                                  390                                  395                                  400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
                                   405                                  410                                  415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
                                   420                                  425                                  430  
 Ser Thr Tyr Lys Gln  
                   435

<210> 497  
 <211> 1080  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1057)  
 <223> RXS02319

<400> 497  
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 agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115  
   Met Ser Asn Tyr Ser  
   1                                  5  
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
                                   10                                  15                                  20  
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
                                   25                                  30                                  35  
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn  
                                   40                                  45                                  50  
 gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac 307  
 Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His  
                                   55                                  60                                  65  
 gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc 355  
 Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly  
                   70                                  75                                  80                                  85  
 ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa 403

aaa	1080
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&lt;210&gt; 498

&lt;211&gt; 319

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 498

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Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
  1          5          10          15

Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
          20          25          30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
          35          40          45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
          50          55          60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
  65          70          75          80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
          85          90          95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
          100          105          110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
          115          120          125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
  130          135          140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
  145          150          155          160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
          165          170          175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
          180          185          190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
          195          200          205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
  210          215          220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
  225          230          235          240

His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
          245          250          255

Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
          260          265          270

Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
  275          280          285

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Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe  
 290 295 300

Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
 305 310 315

<210> 499

<211> 384

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(361)

<223> RXS02908

<400> 499

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gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115  
 Leu Lys Leu His Pro  
 1 5

gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163  
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala  
 10 15 20

tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211  
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala  
 25 30 35

gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259  
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp  
 40 45 50

gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307  
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser  
 55 60 65

ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355  
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys  
 70 75 80 85

ctg ttt tagtcttcat tcttgctggc tgc 384  
 Leu Phe

<210> 500

<211> 87

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 500

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys  
 1 5 10 15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly  
 20 25 30

Arg Ala Ile Ala Lys Leu Phe  
85

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<220>  
<221> CDS  
<222> (101)..(775)  
<223> RXS03003
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<400> 501																	
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caatgatcgc	tgcgctgccg	cctcaggcat	aatctaacgc	atg	acc	tct	cgc	acc	115								
				Met	Thr	Ser	Arg	Thr									
				1				5									
ccg	ctt	gtt	tct	gtt	ctt	cct	gat	ttt	ccg	tgg	gat	tcg	ctc	gct	tcc	163	
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Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
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Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val  
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Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile  
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Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val  
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Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser  
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 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn  
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 His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
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 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
 970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac 3075  
 Val Gly Trp

&lt;210&gt; 508

&lt;211&gt; 984

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 508

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg  
 1 5 10 15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
 20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480  
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val

485										490					495				
Gly	Glu	Val	Ser	Glu	Gln	Asp	Phe	Ser	Thr	Gln	Leu	Val	Ala	Pro	Ser				
			500					505					510						
Glu	Phe	Ala	Ala	Thr	Pro	Val	Pro	Pro	Pro	Met	Ser	Ala	Gly	Ile	Val				
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Arg	Gly	Pro	Arg	Leu	Val	Pro	Gly	Ala	Pro	Val	Gly	Asp	Gly	Arg	Phe				
	530					535					540								
Arg	Leu	Leu	Ala	Asp	His	Gly	Gly	Val	Gln	Gly	Ala	Arg	Phe	Trp	Gln				
545					550					555					560				
Ala	Arg	Glu	Ile	Ala	Thr	Gly	Lys	Glu	Val	Ala	Leu	Ile	Phe	Val	Asp				
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Thr	Ser	Gly	Asn	Ala	Pro	Phe	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Ala	Ala				
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Gly	Ile	Ala	Tyr	Glu	Val	Gln	Arg	Arg	Thr	Lys	Lys	Leu	Ala	Ser	Leu				
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Gly	Ser	Leu	Ala	Val	Ala	Pro	Asn	Ile	His	Ser	Glu	Ala	Tyr	Arg	Asn				
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Gly	Cys	Leu	Ile	Val	Ala	Asp	Trp	Val	Pro	Gly	Ser	Ser	Leu	Ser	Ala				
625					630					635					640				
Val	Ala	Glu	Ser	Gly	Ala	Asp	Pro	Arg	Ala	Ala	Ala	Phe	Ala	Leu	Ala				
				645					650					655					
Glu	Leu	Thr	Glu	Thr	Ile	Gly	Glu	Ala	His	Glu	Met	Gly	Ile	Pro	Ala				
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Gly	Leu	Asp	Asn	Lys	Cys	Arg	Ile	Arg	Ile	Asn	Thr	Asp	Gly	His	Ala				
		675					680					685							
Val	Leu	Ala	Leu	Pro	Ala	Ile	Leu	Pro	Asp	Ala	Ser	Glu	Leu	Arg	Asp				
	690					695					700								
Ala	Lys	Ser	Leu	Ala	Ser	Ala	Ala	Glu	Met	Leu	Ile	Asp	Ala	Thr	Leu				
705					710					715					720				
Ala	Pro	Ser	Asp	Val	Lys	Ala	Met	Val	Thr	Glu	Ala	Gln	Gly	Leu	Ala				
				725					730					735					
Thr	Glu	Asp	Asn	Pro	Asp	Tyr	Ala	Ser	Leu	Ala	Met	Ala	Met	Arg	Thr				
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Cys	Gly	Leu	Phe	Thr	Glu	Glu	Pro	Thr	His	Leu	Val	Val	Lys	Lys	Glu				
		755					760					765							
Lys	Thr	Pro	Lys	Pro	Ala	Thr	Arg	Asp	Gly	Phe	Gly	Ala	Ser	Asp	Tyr				
	770					775						780							
Thr	Val	Lys	Gly	Met	Ala	Ala	Ile	Ala	Ala	Val	Val	Ile	Ile	Leu	Val				
785					790					795				800					
Ser	Leu	Val	Ala	Ala	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Phe	Phe	Gly	Ser				
				805					810					815					

Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser  
 820 825 830  
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
 835 840 845  
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
 865 870 875 880  
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr  
 885 890 895  
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
 900 905 910  
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile  
 915 920 925  
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
 945 950 955 960  
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile  
 965 970 975  
 Ala Glu Val Gln Leu Val Gly Trp  
 980

<210> 509  
 <211> 930  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(907)  
 <223> RXC02080

<400> 509  
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 Met Ser Ile Glu Trp  
 1 5  
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163  
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala  
 10 15 20  
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211  
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
 25 30 35  
 att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac 259

Ile	Leu	Val	Phe	Leu	Gly	Leu	Pro	Pro	Leu	Thr	Ala	Thr	Ile	Ala	Asn	
		40					45					50				
acc	atc	ggc	atc	gtt	cct	gga	agt	att	tcg	ggg	gtg	gtt	gct	tat	aga	307
Thr	Ile	Gly	Ile	Val	Pro	Gly	Ser	Ile	Ser	Gly	Val	Val	Ala	Tyr	Arg	
	55					60					65					
cgt	gaa	cta	cac	gcc	cat	gta	aaa	acc	atc	aga	ttt	ctg	ctg	cca	gca	355
Arg	Glu	Leu	His	Ala	His	Val	Lys	Thr	Ile	Arg	Phe	Leu	Leu	Pro	Ala	
	70				75					80					85	
tca	atc	ctc	gga	ggg	atc	acc	ggc	gcc	tcg	ctc	ttg	ctg	cat	ttc	tcc	403
Ser	Ile	Leu	Gly	Gly	Ile	Thr	Gly	Ala	Ser	Leu	Leu	Leu	His	Phe	Ser	
				90					95					100		
gca	gat	gtt	ttt	aca	gca	gta	att	ccc	tgg	ctg	att	gga	ttc	ggc	acg	451
Ala	Asp	Val	Phe	Thr	Ala	Val	Ile	Pro	Trp	Leu	Ile	Gly	Phe	Gly	Thr	
			105					110					115			
ctg	ttg	gtt	atc	gca	ggg	cca	tca	att	aag	aag	cat	gtt	ggc	gct	cat	499
Leu	Leu	Val	Ile	Ala	Gly	Pro	Ser	Ile	Lys	Lys	His	Val	Gly	Ala	His	
		120					125					130				
act	tca	ggg	ggc	atc	tct	gct	ggg	ttt	agg	caa	ttg	cct	ttc	ccg	agc	547
Thr	Ser	Gly	Gly	Ile	Ser	Ala	Gly	Phe	Arg	Gln	Leu	Pro	Phe	Pro	Ser	
	135					140					145					
cga	acc	acc	ttc	atc	gtc	tca	gta	tgt	ggg	gcc	ctg	ttg	ctg	ggc	atg	595
Arg	Thr	Thr	Phe	Ile	Val	Ser	Val	Cys	Gly	Ala	Leu	Leu	Leu	Gly	Met	
	150				155					160					165	
tat	gga	ggg	tac	ttc	agc	gca	gct	caa	ggc	att	ctt	ctc	atc	gca	ttg	643
Tyr	Gly	Gly	Tyr	Phe	Ser	Ala	Ala	Gln	Gly	Ile	Leu	Leu	Ile	Ala	Leu	
				170					175					180		
ctt	ggc	atc	aca	tca	acg	ctg	cag	atg	cag	gaa	ctc	aac	gcc	atc	aaa	691
Leu	Gly	Ile	Thr	Ser	Thr	Leu	Gln	Met	Gln	Glu	Leu	Asn	Ala	Ile	Lys	
			185					190					195			
aac	ctc	aca	gtg	gcg	gca	gtt	aat	ctc	atc	gca	gcc	agt	gtt	ttt	ata	739
Asn	Leu	Thr	Val	Ala	Ala	Val	Asn	Leu	Ile	Ala	Ala	Ser	Val	Phe	Ile	
		200					205					210				
atc	atc	tcc	cct	gag	ttg	atc	tcc	tgg	ccg	acc	gtt	gcc	tta	atc	gcg	787
Ile	Ile	Ser	Pro	Glu	Leu	Ile	Ser	Trp	Pro	Thr	Val	Ala	Leu	Ile	Ala	
	215					220					225					
ctt	ggc	tca	gct	tta	ggg	gga	tac	atc	ggc	gga	cgg	tac	gcc	cgc	cga	835
Leu	Gly	Ser	Ala	Leu	Gly	Gly	Tyr	Ile	Gly	Gly	Arg	Tyr	Ala	Arg	Arg	
	230				235				240					245		
ctt	cgc	ccc	agt	gtt	ttt	aga	gca	ttt	gtg	gtc	atc	gtc	gga	atc	acc	883
Leu	Arg	Pro	Ser	Val	Phe	Arg	Ala	Phe	Val	Val	Ile	Val	Gly	Ile	Thr	
				250					255					260		
acg	gtc	atc	gtt	atg	acg	atc	ggg	taatgcagca	gactagtaac	ccc						930
Thr	Val	Ile	Val	Met	Thr	Ile	Gly									
				265												

&lt;210&gt; 510



&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 510

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Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
  1           5           10           15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
      20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
      35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
      50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
      65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
      85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
      100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
      115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
      130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
      145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
      165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
      180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
      195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
      210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
      225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
      245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
      260          265

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&lt;210&gt; 511

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                         Met Lys Val Ser Ala
                                         1                               5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                               10                               15                               20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                               25                               30                               35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                               40                               45                               50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                               55                               60                               65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                               70                               75                               80                               85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                               90                               95                               100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                               105                               110                               115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                               120                               125                               130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                               135                               140                               145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                               150                               155                               160                               165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                               170                               175                               180

gga tgaaccaaat ccgaaaccgc cgg 669
Gly

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[illegible]

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<222> (101)..(880)  
<223> RXC02295
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gatgcaagac tgataaccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
                Met Gly Leu Glu Leu
                1             5

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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga	163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg	211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa	499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc	643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg	787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt	835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	
gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg	880

Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
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tagataagtc ggggcaaact cta

903

<210> 514

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
 35 40 45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
 50 55 60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
 65 70 75 80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
 85 90 95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
 100 105 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
 115 120 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
 130 135 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
 145 150 155 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
 165 170 175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
 180 185 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
 195 200 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
 210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
 225 230 235 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
 245 250 255

Ile Gln Gly Met

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<210> 515
<211> 1132
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101) .. (1132)
<223> RXN03063
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Val Glu Asp Leu Ser 5																
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163																
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro 20																
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211																
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala 35																
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259																
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile 50																
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307																
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile 65																
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355																
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val 85																
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403																
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro 100																
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451																
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro 115																
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499																
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala 130																
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547																
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala 145																
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595																
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met 165																
gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643																

Ala Met Thr	Ala Lys Asn Arg Pro Tyr	Lys Ser Gly Phe Gly Pro Leu	
	170	175	180
gcc gca gac gtc	tac cgt gca cca atg tct	tac cca ctg cgc gac gga	691
Ala Ala Asp Val	Tyr Arg Ala Pro Met Ser	Tyr Pro Leu Arg Asp Gly	
	185	190	195
ctg tcc ggc ccg	gaa gcc gca gag cgc gcg	atc tcc gtg atc gaa tcc	739
Leu Ser Gly Pro	Glu Ala Ala Glu Arg Ala	Ile Ser Val Ile Glu Ser	
	200	205	210
cag gtc gga gcc	gaa aac ctc gcc tgc gtg	gtc att gaa ccg atc cag	787
Gln Val Gly Ala	Glu Asn Leu Ala Cys Val	Val Ile Glu Pro Ile Gln	
	215	220	225
ggc gaa ggc gga	ttc atc gtc ccc gca cca	gga ttc ctc gca gcc att	835
Gly Glu Gly Gly	Phe Ile Val Pro Ala Pro	Gly Phe Leu Ala Ala Ile	
	230	235	240
tcc acc tgg tgc	cgc gag aac gac gtg gtg	ttc atc gcc gat gaa atc	883
Ser Thr Trp Cys	Arg Glu Asn Asp Val Val	Phe Ile Ala Asp Glu Ile	
	250	255	260
caa tct ggc ttc	ctg cgc acc ggc gac tgg	ttc gcc agc gac gca gaa	931
Gln Ser Gly Phe	Leu Arg Thr Gly Asp Trp	Phe Ala Ser Asp Ala Glu	
	265	270	275
ggt gtg atc ccc	gac gtc atc acc acc gca	aaa ggc atc gcc ggc ggc	979
Gly Val Ile Pro	Asp Val Ile Thr Thr Ala	Lys Gly Ile Ala Gly Gly	
	280	285	290
atg cca cta tcc	gca gtg acc ggc cgc gca	gaa atc atg gac gca ccc	1027
Met Pro Leu Ser	Ala Val Thr Gly Arg Ala	Glu Ile Met Asp Ala Pro	
	295	300	305
ggc ccc ggc gcg	ctc ggc gga acc tac ggc	gga aac ccc gtt gct tgc	1075
Gly Pro Gly Ala	Leu Gly Gly Thr Tyr Gly	Gly Asn Pro Val Ala Cys	
	310	315	320
gcc gcg gca ctt	gca gcc att gaa gtg atg	gaa caa gcc gac ctt aag	1123
Ala Ala Ala Leu	Ala Ala Ile Glu Val Met	Glu Gln Ala Asp Leu Lys	
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acc cgc gcg			1132
Thr Arg Ala			

&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

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Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala
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Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp
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Ala	Asp	Gly	Gly	Ile	Leu	Ala	Asp	Ala	Asp	Gly	Asn	Arg	Phe	Ile	Asp	
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Leu	Ala	Ser	Gly	Ile	Ala	Val	Thr	Thr	Val	Gly	Gly	Ser	Asn	Ala	Ala	
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Val	Ala	Lys	Ala	Val	Gly	Ala	Ala	Ala	Ala	Arg	Phe	Thr	His	Thr	Cys	
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Phe	Met	Val	Ser	Pro	Tyr	Glu	Thr	Tyr	Val	Ala	Met	Ala	Glu	Arg	Leu	
100					105					110						
Asn	Ala	Leu	Thr	Pro	Gly	Asp	His	Asp	Lys	Lys	Ser	Ala	Leu	Phe	Asn	
115					120					125						
Ser	Gly	Ala	Glu	Ala	Val	Glu	Asn	Ala	Val	Lys	Val	Ala	Arg	Ala	Tyr	
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Thr	Gly	Lys	Gly	Ala	Val	Val	Val	Phe	Asp	Asn	Ala	Tyr	His	Gly	Arg	
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Thr	Asn	Leu	Thr	Met	Ala	Met	Thr	Ala	Lys	Asn	Arg	Pro	Tyr	Lys	Ser	
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Gly	Phe	Gly	Pro	Leu	Ala	Ala	Asp	Val	Tyr	Arg	Ala	Pro	Met	Ser	Tyr	
180					185					190						
Pro	Leu	Arg	Asp	Gly	Leu	Ser	Gly	Pro	Glu	Ala	Ala	Glu	Arg	Ala	Ile	
195					200					205						
Ser	Val	Ile	Glu	Ser	Gln	Val	Gly	Ala	Glu	Asn	Leu	Ala	Cys	Val	Val	
210					215					220						
Ile	Glu	Pro	Ile	Gln	Gly	Glu	Gly	Gly	Phe	Ile	Val	Pro	Ala	Pro	Gly	
225					230					235					240	
Phe	Leu	Ala	Ala	Ile	Ser	Thr	Trp	Cys	Arg	Glu	Asn	Asp	Val	Val	Phe	
245					250					255						
Ile	Ala	Asp	Glu	Ile	Gln	Ser	Gly	Phe	Leu	Arg	Thr	Gly	Asp	Trp	Phe	
260					265					270						
Ala	Ser	Asp	Ala	Glu	Gly	Val	Ile	Pro	Asp	Val	Ile	Thr	Thr	Ala	Lys	
275					280					285						
Gly	Ile	Ala	Gly	Gly	Met	Pro	Leu	Ser	Ala	Val	Thr	Gly	Arg	Ala	Glu	
290					295					300						
Ile	Met	Asp	Ala	Pro	Gly	Pro	Gly	Ala	Leu	Gly	Gly	Thr	Tyr	Gly	Gly	
305					310					315					320	
Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	Leu	Ala	Ala	Ile	Glu	Val	Met	Glu	
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&lt;210&gt; 517



<211> 1491  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1468)  
 <223> RXN02970

<400> 517

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                                     Leu Ala Leu Lys Gly
                                     1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                55                60                65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                70                75                80                85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                105                110                115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                120                125                130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                135                140                145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                150                155                160                165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                170                175                180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser	
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Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys	
		200					205					210				
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala	
	215					220					225					
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro	
230					235					240					245	
gca	ggg	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile	
				250					255					260		
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys	
			265					270					275			
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile	
		280					285					290				
acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc	1027
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile	
	295					300					305					
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Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser	
310					315					320					325	
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag	1123
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys	
			330						335					340		
gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct	1171
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala	
			345					350					355			
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa	1219
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu	
		360					365					370				
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca	1267
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala	
	375					380					385					
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa	1315
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu	
390					395				400						405	
ttc	aag	gaa	cgc	ggc	gtg	tgg	ccg	atg	atc	tcc	ggc	aac	cga	ttc	cac	1363
Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser	Gly	Asn	Arg	Phe	His	
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atc	gcg	ccg	ccg	ctg	acc	acc	act	gat	gac	gaa	ttg	gta	gca	ctg	ctg	1411
Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu	Leu	Val	Ala	Leu	Leu	

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gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459  
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440 445 450

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Ala Leu Phe  
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<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
225 230 235 240



tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala	
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe	
25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala	
40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp	
55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg	
70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn	
90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val	
105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly	
120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly	
135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly	
150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883

Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc  
 Phe Lys Glu Arg Gly  
 410 1330

&lt;210&gt; 520

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 520

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60

Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly	65	70	75	80
His	Asn	Asn	Pro	Arg	Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg	85	90	95	
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	100	105	110	
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	115	120	125	
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	130	135	140	
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	145	150	155	160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	165	170	175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	180	185	190	
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	195	200	205	
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	210	215	220	
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	225	230	235	240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	245	250	255	
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	260	265	270	
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	275	280	285	
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	290	295	300	
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	305	310	315	320
Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	325	330	335	
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	340	345	350	
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	355	360	365	
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	370	375	380	

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Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
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<210> 521

<211> 1998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1975)

<223> RXA01551

<400> 521

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                                         Leu Lys Ala Val Pro
                                         1 5
acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163
Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
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Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
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gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
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ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307
Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu
                        55 60 65
gat gac tcg cca agc ggc ccc aac gaa ccc ttc cgc atc tac cgc acc 355
Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe Arg Ile Tyr Arg Thr
                        70 75 80 85
cgt ggc cca gaa acc aac ccc aag cag gga ctt ccg cgg ctg cgc gag 403
Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu Pro Arg Leu Arg Glu
                        90 95 100
tca tgg atc acc gcc cgc ggc gac gtt gcc acc tat cag ggg cgc gag 451
Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr Tyr Gln Gly Arg Glu
                        105 110 115
cgt ttg ctt atc gac gac ggc cgc tcg gca atg cgt cga ggt caa gct 499
Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala
                        120 125 130
tcg gct gag tgg aaa ggc caa aaa cca gct cct ttg aag gcg cta cct 547
Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro
                        135 140 145
ggc aaa aga gtc acc caa atg gcc tat gca cgt gct ggc gtg att act 595
```



Gly 150	Lys	Arg	Val	Thr	Gln 155	Met	Ala	Tyr	Ala	Arg 160	Ala	Gly	Val	Ile	Thr 165	
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643
Arg	Glu	Met	Glu	Phe 170	Val	Ala	Leu	Arg	Glu 175	His	Val	Asp	Ala	Glu	Phe 180	
gtg	cgc	tct	gag	gtg	gcg	cgc	ggt	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu 185	Val	Ala	Arg	Gly	Arg 190	Ala	Ile	Ile	Pro	Asn	Asn	Val 195	
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggt	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu 200	Ser	Glu	Pro	Met	Ile 205	Ile	Gly	Arg	Lys	Phe	Leu	Thr 210	
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala 215	Asn	Ile	Gly	Asn	Ser 220	Ala	Val	Thr 225	Ser	Ser	Ile	Glu	
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggt	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala 235	Thr	Arg	Trp 240	Gly	Ala	Asp	Thr 245	
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser 250	Thr	Gly	Asp	Asp 255	Ile	His	Thr	Thr	Arg	Glu	Trp 260	
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn 265	Ser	Pro	Val	Pro	Ile 270	Gly	Thr	Val	Pro	Ile	Tyr	Gln 275	
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys 280	Val	Asn	Gly	Val	Ala 285	Ala	Asp	Leu	Asn	Trp	Glu	Val 290	
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	1027
Phe	Arg	Asp	Thr	Ile	Ile	Glu	Gln	Cys 300	Glu	Gln	Gly 305	Val	Asp	Tyr	Met	
acc	atc	cac	gcc	ggc	gtc	ctg	ctg	gct	tat	atc	cca	ctg	act	acc	cgt	1075
Thr	Ile	His	Ala 310	Gly	Val	Leu	Leu	Ala 315	Tyr	Ile	Pro	Leu	Thr	Thr	Arg 325	
cgt	gtc	acc	ggc	att	gtc	tcc	cgc	ggc	gga	tcc	att	atg	gcc	ggt	tgg	1123
Arg	Val	Thr	Gly 330	Ile	Val	Ser	Arg	Gly 335	Gly	Ser	Ile	Met	Ala	Gly	Trp 340	
tgt	ctg	gcg	cat	cac	cgc	gaa	tca	ttc	ctc	tac	gag	cat	ttc	gac	gag	1171
Cys	Leu	Ala	His 345	His	Arg	Glu	Ser	Phe 350	Leu	Tyr	Glu	His	Phe	Asp	Glu 355	
ctg	tgc	gaa	atc	ttt	gca	caa	tat	gac	gtc	gca	ttc	tcc	ctc	ggt	gat	1219
Leu	Cys	Glu	Ile 360	Phe	Ala	Gln	Tyr	Asp 365	Val	Ala	Phe	Ser	Leu	Gly	Asp 370	
ggc	cta	cgc	ccc	gga	tcg	ctt	gcc	gat	gcc	aac	gac	gcc	gcg	caa	ttc	1267
Gly	Leu	Arg	Pro 375	Gly	Ser	Leu	Ala	Asp 380	Ala	Asn	Asp	Ala	Ala	Gln	Phe 385	
gcc	gag	ctg	aaa	acc	att	ggt	gag	ctc	acc	caa	cgc	gcc	tgg	gaa	tac	1315
Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln	Arg	Ala	Trp	Glu	Tyr	

390	395	400	405	
gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg				1363
Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met				
410		415	420	
atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct				1411
Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro				
425	430	435		
ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac				1459
Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp				
440	445	450		
cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc				1507
His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr				
455	460	465		
gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac				1555
Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn				
470	475	480	485	
cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac				1603
Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His				
490	495	500		
gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac				1651
Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp				
505	510	515		
gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg				1699
Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala				
520	525	530		
ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg				1747
Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu				
535	540	545		
ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg				1795
Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro				
550	555	560	565	
aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc				1843
Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly				
570	575	580		
gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt				1891
Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser				
585	590	595		
gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg				1939
Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg				
600	605	610		
gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc				1985
Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg				
615	620	625		
gatcccagat agc				1998



290					295					300					
Gly	Val	Asp	Tyr	Met	Thr	Ile	His	Ala	Gly	Val	Leu	Leu	Ala	Tyr	Ile
305					310					315					320
Pro	Leu	Thr	Thr	Arg	Arg	Val	Thr	Gly	Ile	Val	Ser	Arg	Gly	Gly	Ser
				325					330					335	
Ile	Met	Ala	Gly	Trp	Cys	Leu	Ala	His	His	Arg	Glu	Ser	Phe	Leu	Tyr
			340					345					350		
Glu	His	Phe	Asp	Glu	Leu	Cys	Glu	Ile	Phe	Ala	Gln	Tyr	Asp	Val	Ala
		355					360					365			
Phe	Ser	Leu	Gly	Asp	Gly	Leu	Arg	Pro	Gly	Ser	Leu	Ala	Asp	Ala	Asn
	370					375					380				
Asp	Ala	Ala	Gln	Phe	Ala	Glu	Leu	Lys	Thr	Ile	Gly	Glu	Leu	Thr	Gln
385					390					395					400
Arg	Ala	Trp	Glu	Tyr	Asp	Val	Gln	Val	Met	Val	Glu	Gly	Pro	Gly	His
				405					410					415	
Val	Pro	Leu	Asn	Met	Ile	Gln	Glu	Asn	Asn	Glu	Leu	Glu	Gln	Lys	Trp
			420					425					430		
Ala	Ala	Asp	Ala	Pro	Phe	Tyr	Thr	Leu	Gly	Pro	Leu	Val	Thr	Asp	Ile
		435					440					445			
Ala	Pro	Gly	Tyr	Asp	His	Ile	Thr	Ser	Ala	Ile	Gly	Ala	Ala	His	Ile
	450					455					460				
Ala	Met	Gly	Gly	Thr	Ala	Met	Leu	Cys	Tyr	Val	Thr	Pro	Lys	Glu	His
465					470					475				480	
Leu	Gly	Leu	Pro	Asn	Arg	Asp	Asp	Val	Lys	Thr	Gly	Val	Ile	Thr	Tyr
				485					490					495	
Lys	Leu	Ala	Ala	His	Ala	Ala	Asp	Val	Ala	Lys	Gly	His	Pro	Gly	Ala
			500					505					510		
Arg	Ala	Trp	Asp	Asp	Ala	Met	Ser	Lys	Ala	Arg	Phe	Glu	Phe	Arg	Trp
		515				520					525				
Asn	Asp	Gln	Phe	Ala	Leu	Ser	Leu	Asp	Pro	Asp	Thr	Ala	Ile	Ala	Tyr
	530					535					540				
His	Asp	Glu	Thr	Leu	Pro	Ala	Glu	Pro	Ala	Lys	Thr	Ala	His	Phe	Cys
545					550					555					560
Ser	Met	Cys	Gly	Pro	Lys	Phe	Cys	Ser	Met	Arg	Ile	Ser	Gln	Asp	Ile
				565					570					575	
Arg	Asp	Met	Phe	Gly	Asp	Gln	Ile	Ala	Glu	Leu	Gly	Met	Pro	Gly	Val
			580					585					590		
Gly	Asp	Ser	Ser	Ser	Ala	Val	Ala	Ser	Ser	Gly	Ala	Arg	Glu	Gly	Met
		595					600					605			
Ala	Glu	Lys	Ser	Arg	Glu	Phe	Ile	Ala	Gly	Gly	Ala	Glu	Val	Tyr	Arg
	610					615					620				

Arg  
625

<210> 523  
<211> 1013  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(990)  
<223> RXA01019

<400> 523  
act ttg gcg cac tca ctt tca ttc ccg gat tcg ctt cgc gac ggg cca 48  
Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro  
1 5 10 15  
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag 96  
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
20 25 30  
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat 144  
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
35 40 45  
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192  
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
50 55 60  
ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag 240  
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
65 70 75 80  
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt 288  
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
85 90 95  
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336  
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
100 105 110  
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag 384  
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
115 120 125  
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg 432  
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
130 135 140  
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag 480  
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
145 150 155 160  
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga 528  
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
165 170 175  
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt 576

Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc 624  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga 672  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac 720  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300  
 gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320  
 ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg 1010  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe 330  
 aat 1013

&lt;210&gt; 524

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 524

Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro  
 1 5 10 15

Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
 20 25 30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln

65	70	75	80
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	85	90	95
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	100	105	110
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	115	120	125
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	130	135	140
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	145	150	155
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	165	170	175
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	180	185	190
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	195	200	205
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	210	215	220
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	225	230	235
Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser	245	250	255
Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr	260	265	270
Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu	275	280	285
Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln	290	295	300
Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr	305	310	315
Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe	325	330	

&lt;210&gt; 525

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; RXA01352

&lt;400&gt; 525

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gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60
ctgggtaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
                               Val Phe Glu Asn Arg
                               1                               5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
                               10                               15                               20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val
                               25                               30                               35

cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca 259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala
                               40                               45                               50

tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg 307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val
                               55                               60                               65

ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga 355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly
                               70                               75                               80                               85

ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt 403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu
                               90                               95                               100

gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act 451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr
                               105                               110                               115

gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg 499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu
                               120                               125                               130

gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca 547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser
                               135                               140                               145

ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg 595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu
                               150                               155                               160                               165

tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg 643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val
                               170                               175                               180

cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct 691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala
                               185                               190                               195

ttt tct gaa tct gat 706
Phe Ser Glu Ser Asp
                               200

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&lt;210&gt; 526



&lt;211&gt; 202

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 526

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Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala
  1              5              10              15
Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly
              20              25              30
Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala
              35              40              45
Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
              50              55              60
Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
              65              70              75              80
Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
              85              90              95
Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
              100              105              110
Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
              115              120              125
Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
              130              135              140
Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
              145              150              155              160
Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
              165              170              175
Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
              180              185              190
Ala Met Val Arg Ala Phe Ser Glu Ser Asp
              195              200

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&lt;210&gt; 527

&lt;211&gt; 944

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(921)

&lt;223&gt; RXA01381

&lt;400&gt; 527

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tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac      48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
  1              5              10              15
att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt      96

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Ile	Ser	Asn	Ile	His	Arg	Gln	Ile	Leu	Phe	Gly	Ala	Ser	Asp	Val	Gly	
			20					25					30			
cga	ccc	aag	gtc	gag	gtt	gcc	gcc	gag	cgc	ctc	aaa	gaa	ctc	caa	cca	144
Arg	Pro	Lys	Val	Glu	Val	Ala	Ala	Glu	Arg	Leu	Lys	Glu	Leu	Gln	Pro	
		35					40					45				
gac	atc	acc	gtc	aac	gcg	ttg	cac	gaa	cgg	atc	act	cca	gaa	aac	gcc	192
Asp	Ile	Thr	Val	Asn	Ala	Leu	His	Glu	Arg	Ile	Thr	Pro	Glu	Asn	Ala	
	50					55					60					
tgc	gag	ctg	ctc	aat	tcc	gtg	gac	ctc	gtc	tta	gac	ggc	tcc	gat	tct	240
Cys	Glu	Leu	Leu	Asn	Ser	Val	Asp	Leu	Val	Leu	Asp	Gly	Ser	Asp	Ser	
	65				70					75					80	
ttc	tcc	aca	aaa	tac	tta	gtg	tct	gat	gcc	gcc	gaa	atc	acc	gga	act	288
Phe	Ser	Thr	Lys	Tyr	Leu	Val	Ser	Asp	Ala	Ala	Glu	Ile	Thr	Gly	Thr	
				85					90					95		
ccc	ctc	atc	tgg	gca	acg	gta	ctg	cgc	ttt	cac	ggc	gaa	ctg	gca	ctc	336
Pro	Leu	Ile	Trp	Ala	Thr	Val	Leu	Arg	Phe	His	Gly	Glu	Leu	Ala	Leu	
			100					105					110			
ttc	aac	tct	ggc	ccc	gac	cac	cgc	gga	gtc	ggc	ctg	cgc	gac	gtc	ttc	384
Phe	Asn	Ser	Gly	Pro	Asp	His	Arg	Gly	Val	Gly	Leu	Arg	Asp	Val	Phe	
		115					120					125				
ccc	gaa	caa	ccc	tcc	gcc	gat	ttc	gtc	cct	gac	tgc	gcc	acc	gct	ggt	432
Pro	Glu	Gln	Pro	Ser	Ala	Asp	Phe	Val	Pro	Asp	Cys	Ala	Thr	Ala	Gly	
	130					135					140					
gtt	ctt	ggc	gcc	acc	aca	gcc	acc	atc	ggc	gca	ctc	atg	gcc	act	cac	480
Val	Leu	Gly	Ala	Thr	Thr	Ala	Thr	Ile	Gly	Ala	Leu	Met	Ala	Thr	His	
	145				150					155					160	
gcc	atc	gga	ttt	ctc	aca	gaa	atc	ggc	gac	gtc	caa	cca	ggc	aca	atc	528
Ala	Ile	Gly	Phe	Leu	Thr	Glu	Ile	Gly	Asp	Val	Gln	Pro	Gly	Thr	Ile	
				165					170					175		
ctc	tcc	tac	gac	gca	ttc	ccc	gcc	gcc	acg	cgc	agc	ttc	cgc	gtc	tcc	576
Leu	Ser	Tyr	Asp	Ala	Phe	Pro	Ala	Ala	Thr	Arg	Ser	Phe	Arg	Val	Ser	
			180					185					190			
gcc	gac	cgc	gcg	cgc	cca	ctg	gtc	acc	cgc	ctc	cgc	gcc	tcc	tac	gag	624
Ala	Asp	Pro	Ala	Arg	Pro	Leu	Val	Thr	Arg	Leu	Arg	Ala	Ser	Tyr	Glu	
		195				200						205				
gca	gcg	cgc	acc	gat	aca	act	tcg	ctt	atc	gac	gcc	acc	ctc	aac	ggc	672
Ala	Ala	Arg	Thr	Asp	Thr	Thr	Ser	Leu	Ile	Asp	Ala	Thr	Leu	Asn	Gly	
	210					215					220					
tcc	ctc	acc	gcc	ctc	gat	atc	cga	gag	cca	cat	gaa	gtt	ctg	ctc	aaa	720
Ser	Leu	Thr	Ala	Leu	Asp	Ile	Arg	Glu	Pro	His	Glu	Val	Leu	Leu	Lys	
	225				230					235					240	
gac	ctc	ccc	gag	ggc	gca	acg	tca	ctg	aag	ctc	ccc	tta	agc	cag	atc	768
Asp	Leu	Pro	Glu	Gly	Ala	Thr	Ser	Leu	Lys	Leu	Pro	Leu	Ser	Gln	Ile	
				245					250					255		
acc	tcg	gac	agc	gac	att	tta	gag	gca	ctg	tct	gga	atc	gac	ggc	gac	816
Thr	Ser	Asp	Ser	Asp	Ile	Leu	Glu	Ala	Leu	Ser	Gly	Ile	Asp	Gly	Asp	

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                260                265                270
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac 864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
      275                280                285

aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc 912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
      290                295                300

aac gcg ctg tagctgtcaa tttaagaggc cag 944
Asn Ala Leu
305

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&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

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Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
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Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
      20                25                30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
      35                40                45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
      50                55                60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
      65                70                75                80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
      85                90                95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
      100                105                110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
      115                120                125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
      130                135                140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
      145                150                155                160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
      165                170                175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
      180                185                190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
      195                200                205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly

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210	215	220
Ser Leu Thr Ala Leu Asp 225	Ile Arg Glu Pro His 230	Glu Val Leu Leu Lys 235 240
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys 245	Leu Pro Leu Ser Gln Ile 250	
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp 260		270
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp 275	280	285
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val 290	295	300
Asn Ala Leu 305		

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA01360

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 gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115  
 Met Leu His Ile Ala  
 1 5  
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20  
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35  
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu  
 40 45 50

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala

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Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr					
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Thr Ser Ser Gly Glu					
	50				

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 <212> DNA  
 <213> Corynebacterium glutamicum

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acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc	288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
 165 170 175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt 576  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
 180 185 190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga 626  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
 195 200

tta 629

&lt;210&gt; 532

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 532

Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val  
 1 5 10 15

Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
 20 25 30

Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
 35 40 45

Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
 50 55 60

Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
 65 70 75 80

Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
 85 90 95

Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
 100 105 110

Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
 115 120 125

Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
 130 135 140

Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
 145 150 155 160

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
 165 170 175

Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
 180 185 190

Asp Val Cys Asp Pro Phe Arg His Gln Ile  
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&lt;210&gt; 533

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Val Ala Asn Ser Phe 1 5															
ттg gat tct тta act cтт gтт cga caa aac act ccc cтт gтт cag тgt 163															
Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr Pro Leu Val Gln Cys 10 15 20															
ттg acc aac tct gtg gtc atg caa тtc acg gcc aat gtg тtg cтт gcc 211															
Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala Asn Val Leu Leu Ala 25 30 35															
gcg ggt gcg acc cct gcg atg gtg gat act cca gct gaa tcg gca gaa 259															
Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro Ala Glu Ser Ala Glu 40 45 50															
ттc gcc gct gtg gcc aat gga gtg ctc atc aat gcg gga act cct tct 307															
Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn Ala Gly Thr Pro Ser 55 60 65															
gcg gag caa tac caa ggc atg acc aag gcc att gag ggt gca cga aaa 355															
Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile Glu Gly Ala Arg Lys 70 75 80 85															
gct ggc aca cca тgg gtg тta gac cca gтт gct gtg ggt ggg тtg tcg 403															
Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala Val Gly Gly Leu Ser 90 95 100															
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Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp Lys Gln Pro Ala Ala 105 110 115															
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Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu Ala Gly Leu Gly Ala 120 125 130															
ggt ggg cgc ggc gta gac gcg acc gat тcc gtg gaa gtg gcg тtg gag 547															
Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val Glu Val Ala Leu Glu 135 140 145															
gcg gcg caa тtg тtg gcc aag cgc act ggt ggc gtc gtg gct gtc tct 595															
Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly Val Val Ala Val Ser 150 155 160 165															
ggt gcg gag gac тtg att gtg tct gcg gat cgg gtg acg тgg тtg cgt 643															
Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg Val Thr Trp Leu Arg 170 175 180															
tcg ggg gat ccg atg тtg cag ctg gtg att ggc act gga тgc tct тtg 691															

Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly Thr Gly Cys Ser Leu  
 185 190 195

ggc gcg ctg aca gct gca tat cta ggc gcc acg gtt gac tca gat att 739  
 Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr Val Asp Ser Asp Ile  
 200 205 210

tcc gcg cac gat gct gtg ttg gct gcg cat gcc cat gtg ggt gct gct 787  
 Ser Ala His Asp Ala Val Leu Ala Ala His Ala Val Gly Ala Ala  
 215 220 225

ggc cag att gca gca cag aag gca tcg gcg cca ggc agc ttt gcg gtg 835  
 Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro Gly Ser Phe Ala Val  
 230 235 240 245

gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883  
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser  
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 Leu Val Asp Val Arg Glu Ala  
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<210> 534  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala  
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Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro  
 35 40 45

Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn  
 50 55 60

Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile  
 65 70 75 80

Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala  
 85 90 95

Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp  
 100 105 110

Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu  
 115 120 125

Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val  
 130 135 140

Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly  
 145 150 155 160

Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg



	165		170		175
Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly	180		185		190
Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr	195		200		205
Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala	210		215		220
His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro	225		230		235
Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala	245		250		255
Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala	260		265		

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(1000)  
 <223> RXA00838

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 Met Lys Ile Ala Ile 1 5  
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu 10 15 20  
 tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala 25 30 35  
 ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr 40 45 50  
 gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307  
 Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp 55 60 65  
 gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355  
 Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala 70 75 80 85  
 gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403  
 Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln 90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451  
 Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
 105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499  
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro  
 120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547  
 Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp  
 135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg 1023  
 Lys Glu Glu Glu Asn Ser Leu  
 295 300

&lt;210&gt; 536

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly

1	5	10	15
Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly	20	25	30
Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala	35	40	45
Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu	50	55	60
Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg	65	70	75
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

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                                         Met Ser Ile Ser Arg
                                         1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
                        10 15 20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
                        25 30 35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
                        40 45 50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
                        55 60 65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
                        70 75 80 85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
                        90 95 100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
                        105 110 115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
                        120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
                        135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
                        150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
                        170 175 180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
                        185 190

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tca

693

&lt;210&gt; 538

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu  
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Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro  
 20 25 30

Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser  
 35 40 45

Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro  
 50 55 60

Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp  
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Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly  
 85 90 95

Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val  
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Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu  
 115 120 125

Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr  
 130 135 140

Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys  
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Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly  
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Phe Arg Asp Val Ala Glu Val Pro Val Thr Phe Ala Ala Ala  
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&lt;210&gt; 539

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; RXN01209

&lt;400&gt; 539

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro



tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
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Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
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Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
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Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	1123
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly	
330 335 340	
tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc	1171
Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr	
345 350 355	
agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc	1219
Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg	
360 365 370	
ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc	1267
Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala	
375 380 385	
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Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala	
390 395 400 405	
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Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys	
410 415 420	
ggg gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc	1411
Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro	
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gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac	1459
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Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile	
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gcc gcc ggc gaa agc gtg gaa	1528
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&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
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Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Lys Glu Leu Lys
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Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
          65          70          75          80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
          85          90          95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
          100          105          110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
          115          120          125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
          130          135          140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
          145          150          155          160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
          165          170          175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
          180          185          190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
          195          200          205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
          210          215          220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
          225          230          235          240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
          245          250          255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
          260          265          270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
          275          280          285

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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Leu Thr 290  
 Phe Leu Gln Gln Leu Gln Ala Val Phe Ser Asp Val Thr Val Asp 305  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val 320  
 Ala Ser Trp Leu Gly Ser His Gln His Gly Pro Val Val Leu Asp Pro 335  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Gln 350  
 Gln Ser Leu Arg Arg Leu Ala Val His Val Asp Val Thr Pro Asn 365  
 Ile Pro Gln Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met 385  
 Asp Gln Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr 400  
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn 415  
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Gln Asn Leu Arg 430  
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 Met Cys Gln Arg Pro 5  
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 Gln Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val 20  
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 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile 35  
 25 30

259	tcc ggc gga gtt tct gtg gtg cag ctc ggc gat aag aac tca ggc gtg	Ser Gly Val	40	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	55	50
307	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	55	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	65	307
355	cgc ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt ggc ggt	Arg Gly Val Ala Leu Val Val Val Val Val Val Val Val Val	70	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	80	355
403	ctg ggt ctt cac ctg ctt ggt ctt ggt ctt ggt ctt ggt ctt ggt	Leu Gly Leu His Leu His Leu His Leu His Leu His Leu His Leu	90	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	95	403
451	gca cgg gag ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	Ala Arg Glu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu	105	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	110	451
499	aac ctg gat caa ttg cat gct gtc gtc gtc gtc gtc gtc gtc gtc	Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	120	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	130	499
547	gtg gca ttg ccc gat gtg att ggc att ggc att ggc att ggc att	Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	140	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	145	547
595	acc aaa cca gat ggc gca ccc gca ttg ggt ggt ggt ggt ggt ggt	Thr Lys Pro Asp Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	155	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	160	595
643	atc gcc gct gta gct caa gac cac gac gac gac gac gac gac gac	Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	170	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	175	643
691	ggc gtt ggt cta cgc aac ggc ggc gaa ctc gct gct gct gct gct	Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Thr Pro Ile Asp	185	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	190	691
739	ggt ctg tgc gtc gtc tct gaa atc atg acc gcc gcc gcc gcc gcc	Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	200	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	210	739
787	ggc gca act cgc ctg cgg act gct ttt caa cct act ttc tgc cct gaa	Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	220	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	225	787
835	act caa act gaa ctc tct caa acc gaa ctc gaa ggc ttc gtg aat	Thr Gln Thr Glu Leu Ser Gln Thr Gln Leu Glu Gly Ala Phe Val Asn	235	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	240	835
883	tgc cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	250	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	255	883
931	ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	265	gaa gat gtt cgt gcg gca gca aag gag ctc aaa gaa ctc tgc gat gct	Glu Asp Val Arg Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	270	931

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Ala Ala Gly Glu Ser Val Glu  
470 475

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile	20	25	30
Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp	35	40	45
Lys Asn Ser Gly Val Gln Asp Val Arg Ala Ala Lys Gln Leu Lys	50	55	60
Gln Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu	65	70	75
Asp Ile Ala Val Gln Leu Gly Leu His Ile Gly Gln Gly Asp	85	90	95
Thr Pro Tyr Thr Gln Ala Arg Gln Leu Pro Ala His Leu Gln Leu	100	105	110
Gly Leu Ser Ile Gln Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln	115	120	125
Cys Ala Gln Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro	130	135	140
Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val	145	150	155
Gln Gly Ile Ala Gln Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala	165	170	175
Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Gln Leu Ala	180	185	190
Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Gln Ile Met Thr Ala	195	200	205
Ala Asn Pro Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro	210	215	220
Thr Phe Ser Pro Gln Thr Gln Thr Gln Leu Ser Gln Thr Gln Leu Gln	225	230	235
Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala	245	250	255
Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser	260	265	270
Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val	275	280	285
Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr	290	295	300
Phe Leu Gln Gln Gln Leu Gln Ala Val Phe Ser Asp Val Thr Val Asp	305	310	315
Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val	325	330	335

Ala Ser Trp Leu Gly Ser His Gln His Gly Pro Val Val Leu Asp Pro 340  
Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Gln 355  
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn 370  
Ile Pro Gln Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met 385  
Asp Gln Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr 405  
Ile Val Ile Val Lys Gly His Leu Thr Gly Ala Leu Ala Asp Asn 420  
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Gln Asn Leu Arg 435  
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Leu Thr His Leu Phe 1  
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Leu Gln Leu Asp Gln Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr 20  
caa tgg act gag cat tlg ttc cgg ctg cca ctg caa cat ctc cgt aac 211  
Gln Trp Thr Gln His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn 35  
tcg ccc aat gac ctg cag gga tlg aag ata cga tgg tgt gaa ctc tat 259  
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Gln Leu Tyr 50  
tcc aca acg ggg aaa gat caa ggg gta gaa ctc ctg cct caa gca acc 307  
Ser Thr Thr Gly Lys Asp Gln Gly Val Gln Leu Leu Pro Gln Ala Thr 65

gtc gtc acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctc gag  
 Val Val Thr Pro Asn Asn Phe Gln Ala Ser Thr Leu Ser Gly Leu Gln  
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 Lys Leu Gln Thr Val Gln Asp Leu Lys Gln Ala Ala Arg Leu Ile Tyr  
 403 90 95  
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 Gln Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro  
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 Gly Gln Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val  
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Ala Arg Leu Ile Tyr Gln Gln Gly Pro Gln Tyr Val Val Lys Gly 100  
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Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Gln Leu Ala 145  
Lys Gly Ala Gln Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val 165  
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Leu Ile Leu Lys Thr 1  
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Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn 20  
cag att gag gcc acc gca gca gca gca gca gca gca gca gca gca gca 211  
Gln Ile Gln Ala Ala Thr Ala His Asp Leu Asp Val Val Lys Ile 35  
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Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu 50  
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307  
Gln Gln Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys 65  
aag ggc cag gag ccc ggc gca ctc gat act gac act gcc ctc cgc 355  
Lys Gly Gln Gln Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg 85  
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Pro Gln Tyr Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn  
130 135 140  
Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Gln  
145 150 155  
Pro Lys Ile Gly Asp Gln Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
165 170 175  
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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
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144 35 40 45  
Ala Leu Gln Gln Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu  
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192 50 55 60  
Ile Cys Lys Gly Gln Gln Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala  
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac  
240 65 70 75 80  
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn  
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac  
288 Phe Gln Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Gln Thr Ile Asp

85 90 95

336 gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac  
 Asp Leu Lys Glu Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr

384 gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac  
 Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp

432 gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile

480 ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc  
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Val Ile

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625 gca cag ttt acc tct gtg tgg tgg gca gtc ggc gaa gac aac aag tagaatcct  
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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr

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Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Thr Ile Asp

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr

Val Val Val Lys Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

115 120 125  
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Gln Pro Lys Ile  
 130 135 140  
 Gly Asp Gln Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Val Ile  
 145 150 155  
 Thr Ala Gln Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
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 115 Met Pro Ser Ala Gly  
 1 15 20  
 gag gag att tta gag cag cgc gca cag ctg gag ttg gat cag cgc cgc  
 163 Gln Gln Ile Leu Gln Arg Ala Gln Leu Gln Phe Asp Gln Arg Arg  
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 gcc gat gtg gtg atg atc gcc agc cag cag gtg gtt tat ggt tcc gtc ggg  
 211 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
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 ctg agt gct gcc att ccg gtg atg cac aac gaa ggc ctg cgc gtc gtc  
 259 Leu Ser Ala Ala Ile Pro Val Met His Asn Gln Gly Leu Arg Val Val  
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 307 Ala Val Pro Thr Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser  
 55 60 65  
 cac cgc cag cag ccg atg tcg gac caa tgg ctg gcc gac ggc tcg caa gac  
 355 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp  
 70 75 80 85  
 ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc  
 403 Leu Val Asp Leu Gly Ile Ile Asp Gln Val Ser Thr Ile Ser Thr Gly  
 90 95 100  
 tat ttt acc tcc gct tct cag gtg cgt gtc gct gct gtc gtc cag  
 451 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Trp Leu Gln

499	aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gat ccc atc	lys ile arg glu thr his pro his val arg ile val val asp pro ile	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260
547	atg ggg gac agt gac gtg gga atc tat gtc gcc gac gag atc gca acc	met gly asp ser asp val gly ile tyr val ala asp glu ile ala thr	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275
595	gcc atc tgc cag gac tca tgc cct ctg gct acc gga atc atc ccc aat	ala ile cys gln asp leu cys pro leu ala thr gly ile pro asn	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290
643	gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tgc ctg	ala phe glu leu ser his met val gly ser gly asp pro arg ser leu	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310
691	ctc ggc ccg ttt ggc gag tgg atc atc atc atc atc atc atc atc atc	leu gly pro phe gly glu trp ile ile ile ile ile thr ser ala thr glu thr	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325
739	gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa	val gly thr thr val thr arg asp ser val gln glu	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340
787	atc gcc tcc gcc acc gtc gat acc acc ggc aaa ggg gca ggc gag gtc	ile ala ser ala thr val asp thr thr ala lys gly asp val	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355
835	tac gcc gca gca tta atc gcc gtc cat aaa gat ttt tgc ctt atc	tyr ala ala ala leu ile ala leu his lys asp phe ser leu ile	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370
883	gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc	asp ala ala ser his ala ser asn thr val cys ala gly leu gln thr	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390
915	aaa gcg ctt tagttcgt ccgtctcga cag	lys ala leu	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430

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 <213> Corynebacterium glutamicum

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 25  
 30  
 tyr gly ser val gly leu ser ala ala ile pro val met his asn glu  
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 45  
 gly leu arg val val ala val pro thr val val leu ser ser met pro  
 50  
 55  
 60



211	Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ser Lys Gln Ala	25	30	35		
259	tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct	Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln Trp Ala Arg Thr Ala	40	45	50	
307	gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc	Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile Asn Ala Leu Asn Val	55	60	65	
355	ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg	Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met	70	75	80	85
403	aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg gat gtc	Thr Ala Ala Leu Asp Gln Ala Leu Lys Leu Gly Gln Leu Gly Asp Val	90	95	100	
451	gca agg att act gag gct ttg gct gtt ggt tct gtt gct gga gcc cga	Ala Arg Ile Thr Gln Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg	105	110	115	
499	gga aat tct gga gta gta gtc ctt agt cag gtc ctt gcg gct att gct cag	Gly Asn Ser Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln	120	125	130	
547	gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta	Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Gln Ala Leu	135	140	145	
595	tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag	Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Gln	150	155	160	165
622	ggc act gtt gtc act gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt gtt	Gly Thr Val Val Thr Val Leu Arg Ser	170			
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35	Ala Ser Lys Gln Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln	Ala Ser Lys Gln Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Gln	35	40	45	
50	Trp Ala Arg Thr Ala Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile	Trp Ala Arg Thr Ala Val Gln Gln Leu Ser Gln Arg Arg Ala Gln Ile	50	55	60	
65	Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn	Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn	65	70	75	80



[illegible]



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<211> 328  
<212> PRT  
<213> Corynebacterium glutamicum

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Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gln  
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Gly	Pro	His	Ala	Glu	Val	Val	Ala	Leu	Ala	Ala	Gly	Val	Arg	Ala	50
Asn	Gly	Gly	Thr	Ala	Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	65
Arg	Thr	Gly	Pro	Cys	Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	85
Val	Phe	Tyr	Ala	Asn	Ala	Asp	Pro	Phe	Pro	Ser	Ala	Gly	Gly	Gly	100
Ala	Phe	Leu	Ala	Glu	Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	115
Ile	Arg	Ala	Leu	Glu	Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	130
His	Val	Thr	Leu	Lys	Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	145
Thr	Asp	Gly	Thr	Ser	Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	165
Val	His	Glu	Asp	Arg	Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	180
Thr	Ala	Leu	Thr	Asp	Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	195
Leu	Tyr	Glu	Asn	Gln	Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	210
Pro	Ala	Asp	Ser	Asn	Leu	Ala	Arg	Leu	Gly	Tyr	Gln	Gln	Tyr	Ala	225
Ile	Pro	Glu	Ala	Leu	Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	245
Leu	Ile	Glu	Gly	Gly	Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	260
Ile	Val	Asp	Gln	Val	Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Gly	Ala	275
Gly	Arg	Ser	Val	Ile	Asn	Trp	Pro	Gln	Gln	Thr	Thr	Met	Asp	Gln	290
Met	Arg	Phe	Asp	Thr	Thr	Ser	Val	Arg	Gln	Leu	Gly	Ser	Asp	Val	305
Ile	Glu	Met	Met	Arg	Lys	Glu	His								325

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<212> DNA  
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Met Phe Thr Gly Ile  
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gac gag gag ctt ggc tcc gtt gca ggc gttg gaa cat ctg gga gat tcc  
Val Glu Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Asp Ser  
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atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gttg cat ttg  
Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
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ggg gat tcc att tct gtc aat ggt gttg tgc ttg aca gttg ggc tcc ttt  
Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
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ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc  
Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
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agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc  
Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
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gac atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat  
Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
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ggt gat gcc acc acc tgc atc aag cgc acc agc tca gag aac tgg  
Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Ser Glu Asn Trp  
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gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gttg gttg  
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
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Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
130

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc  
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
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gac acc acc ccc ggc gaa ctg gcg gta ggg gat atc gta aac att gag  
Asp Thr Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
160

ggt gat gttg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gttg  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
175

ggt gat gttg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gttg  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
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756

733

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gct gga aac act ccc aat gac tac acc gat ttc acg aga gac  
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<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

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25  
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Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
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45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
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55  
60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
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70  
75  
80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
85  
90  
95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
100  
105  
110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
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120  
125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
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Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
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160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
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Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
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Thr Arg Asp  
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<212> DNA

GenBank accession number: F01111.1  
Corynebacterium glutamicum strain ATCC 13035

<213> Corynebacterium glutamicum

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<223> RXN02248

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115 Val Ser Gln His Gln  
1 Val

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gag atc  
163 Gln Ala His Ser Gln Leu Asp Ser Val Gln Ala Ile Ala Asp Ile  
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gct gcg ggt aaa gcc gtc gtc gtc gta gat gat gaa gat cgt gaa aat  
211 Ala Ala Gln Lys Ala Val Val Val Val Val Val Val Val Val Val  
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gaa ggc gac atc atc ttc gcc gcc gaa tta gcc act cca gaa tta gtc  
259 Gln Gln Asp Ile Ile Phe Ala Ala Gln Leu Ala Thr Pro Gln Leu Val  
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gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc  
307 Ala Phe Met Val Arg Tyr Ser Ser Gln Tyr Ile Cys Ala Pro Leu Thr  
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gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat  
355 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Met Thr Ala His Asn  
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cag gat gcc gcc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc  
403 Gln Asp Ala Arg Gln Tyr Thr Val Thr Val Thr Val Thr Val Thr  
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ggc acc aca ggc att tct gca aca gac gcg gcc cac act ttc gct ttc  
451 Gly Thr Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
115

ctt gct gat cca gaa gcc gac gcg acg gat ttc acc cgt ccc gga cac  
499 Leu Ala Asp Pro Gln Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
130

gct gtg cca cta cgt gct gct gaa ggt ggc gtc gtc gtc gtc gtc gtc  
547 Val Val Pro Leu Arg Ala Arg Gln Gly Val Leu Val Arg Ala Gly  
145

cac acc gaa gaa gca gct gtc gat ttc gtc gtc gtc gtc gtc gtc gtc  
595 His Thr Gln Ala Ala Val Asp Leu Ala Arg Ala Gly Leu Arg Pro  
165

gca ggt gtt atc tgc gaa gtc gtc agt gaa gag gac gcc acc ggc atg  
643 Ala Gly Val Ile Cys Gln Val Val Ser Gln Gln Asp Pro Thr Gly Met  
180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag  
691 Ala Arg Val Pro Gln Leu Arg Arg Arg Phe Cys Asp Gln His Asp Lys  
195

739	ctg atc tct atc gaa cag ctc att gaa tgg cgt cgc aag aat gaa att	200	Leu Ile Ser Ile Gln Gln Leu Ile Gln Trp Arg Lys Asn Gln Ile	210
787	ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg	215	Leu Val Gln Arg Gln Val Thr Val Leu Pro Thr Asp Phe Gly Thr	225
835	ttc aag gct gtc ggt tac cgt tcc att ctc gat ggc acc gag ctt gtt	230	Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Gln Leu Val	245
883	ggc att gtt ggc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg	250	Ala Ile Val Val Ala Gly Asp Val Ala Ser Asp Gly Gln Asn Val Leu	260
931	gtt cga gtc ctc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg	265	Val Arg Val His Ser Gln Cys Leu Thr Gly Asp Val Phe Gly Ser Arg	275
979	cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag	280	Arg Cys Asp Cys Gly Gln Gln Leu His Gln Ser Leu Arg Leu Ile Gln	290
1027	gaa gct ggt cgg gga gta gta gta gta gta gta gta gta gta gta gta	295	Gln Ala Gly Arg Gly Val Val Val Val Val Val Val Val Val Val	305
1075	ggc att ggt ctg ctc ggc aag cta cgc ggc tac caa ctc cag gat gaa	310	Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Asp Gln	325
1123	ggt ggc gac acc gtc gat ggc aac ctc gca ctt ggt ctt cca gcc gat	330	Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp	340
1171	ggc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg	345	Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val	355
1219	cgc tgc ctc aac ttg atc agc aac cca gcc aag aag gtg gga ctt	360	Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu	370
1267	gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct	375	Gln Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala	385
1315	ggt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg	395	Val His Gln Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met	405
1363	gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa	410	Gly His Asp Leu Pro Asp Val Ala Leu Trp Gln Gln His Pro Gln	420
1389	aac taaggagcac aacaaatgct aaa			





Leu Arg Leu Ile Gln Gln Ala Gly Arg Gly Val Val Tyr Met Arg 290  
 305 Gly His Gln Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr 320  
 Gln Leu Gln Asp Gln Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu 335  
 Gly Leu Pro Ala Asp Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu 340  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala 355  
 Lys Lys Val Gly Leu Gln Gly His Gly Ile Ser Ile Ala Ser Arg Thr 370  
 Pro Ile Pro Val Ala Val His Gln Asp Asn Val Arg Tyr Leu Lys Thr 385  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Gln 405  
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 Gln Gln His Pro Gln Asn 420  
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 <223> FRXA02248  
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 Val Ser Gln His Gln 1  
 5  
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Gln Gln Ala Ile Ala Asp Ile 20  
 gct gcg ggt aaa gcc gtc gtc gtc gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Val Val Val Val Val Val 30  
 gaa gcc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Gln Gly Asp Ile Ile Phe Ala Ala Gln Leu Ala Thr Pro Gln Leu Val 50  
 gct ttc atg gtg cgt tat tcc tcc gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr 65  
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1123	ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat	Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gln Leu Pro Ala Asp	340	
1171	gcc cgc gaa ttg ggc acc agc gcc cag att ctg tac gag ttg ggt gtg	Ala Arg Gln Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val	355	
1219	cgc tcg ctc aac tgg atc agc aac aac cga gcc aag aag gtg gga cct	Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu	360	
1267	gaa ggc cac ggc att tcc att gcc agc cga acc ccc att cct gtt gct	Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala	385	
1315	glt cat gaa gac aat gtc cga tac cta aaa acc aag cgt gag cgc atg	Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met	400	
1363	gga cat gac ctc cca gat gtc gca ctg tgga caa gag cac gga gaa	Gly His Asp Leu Pro Asp Val Ala Leu Trp Gln Gln His Pro Gln	415	
1389	aac taaggagcac aaccaatggct aaa	Asn	420	
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Glu Asp Arg Gln Asn Gln Gly Asp Ile Ile Phe Ala Ala Gln Leu Ala	35			
Thr Pro Gln Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile	50			
Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro	65			
Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr	85			
Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala	100			
His Thr Leu Arg Leu Leu Ala Asp Pro Gln Ala Asp Arg Thr Asp Phe	115			

1000 900 800 700 600 500 400 300 200 100 0

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Gly Gly Val	130	135	140
Leu Val Arg Ala Gly His Thr Glu Ala Val Asp Leu Ala Arg Ala	145	150	155
Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu	165	170	175
Asp Pro Thr Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp	180	185	190
Glu His Asp Leu Lys Leu Ile Ser Ile Glu Glu Leu Ile Glu Trp Arg	195	200	205
Arg Lys Asn Glu Ile Leu Val Glu Arg Glu Val Thr Val Leu Pro	210	215	220
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp	225	230	235
Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly	245	250	255
Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp	260	265	270
Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Glu Glu His Glu Ser	275	280	285
Leu Arg Leu Ile Glu Glu Ala Gly Arg Gly Val Val Tyr Met Arg	290	295	300
Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr	305	310	315
Gln Leu Glu Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu	325	330	335
Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Glu Ile Leu	340	345	350
Tyr Asp Leu Gly Val Arg Ser Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala	355	360	365
Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr	370	375	380
Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr	385	390	395
Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu	405	410	415
Gln Glu His Pro Glu Asn	420		

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<212> DNA  
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<223> RXN02249

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Met Ala Lys Gln Gly  
1

tgc ccg gca gtc gaa ctc gcc gac gcc agc gga tta aaa gtc gcc gta 163  
Leu Pro Ala Val Gln Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc cgc ctc aag cac 211  
Val Thr Ala Arg Trp Asn Ala Gln Ile Cys Asp Arg Leu His Lys His  
25 30 35

gca gta gat gat gcg gga cgt gca gga gca gga acg gtc agc gaa tac cgc 259  
Ala Val Asp Ala Gly Arg Ala Gly Ala Thr Val Ser Gln Tyr Arg  
40 45 50

gtc atc gcc ggc ctc gaa ctc cca gtc gta gtc caa gaa ctc gca cgc 307  
Val Ile Gly Ala Leu Gln Leu Pro Val Val Val Gln Leu Ala Arg  
55 60 65

acc cat gac gca gta gtc gcc tgc ggc tgc gtc gtc gtc ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtc tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Gln Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtc tgc act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gaa gag caa gcc gtc gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Gln Gln Ala Val Gln Arg Ser Gly Gly Gln Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Gln Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaagtc 597  
Val Leu Ser Gln Ile Arg Ala Thr Gln Gly  
150 155

ctg

600

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<211> 159  
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<213> Corynebacterium glutamicum

<400> 564  
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20 25 30  
Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Thr  
35 40 45  
Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val  
50 55 60  
Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
65 70 75 80  
Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
85 90 95  
Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
100 105 110  
Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
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Met Ala Lys Glu Gly  
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163  
ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta  
Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
20  
gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac  
Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
25 30 35  
gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc  
Ala Val Asp Ala Gly Arg Ala Gly Ala Thr Val Ser Glu Tyr Arg  
259





115 120 125

Gly Gln Gly Ser Val Gln Asp Lys Gly Ala Gln Ala Met Val Ala Ala  
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 115 Val Thr Thr Asn Ala  
 1 Val  
 ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc  
 163 Pro Asp Gly Ala Thr Asn Ile Asn Asn Ala His Ser Gly Ala Val  
 20 15  
 ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc  
 211 Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Gln Ile Gln Gln Tyr Thr  
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 gca gct ttc gct ggc acc acc acc acc acc aag cca tgg gag ctg gag gtc  
 259 Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Gln Leu Val  
 50  
 acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtc gtc gtc atc  
 307 Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Ile  
 55  
 atg gcc gct cac atc ttc atg ggt gcc gtc gtc gac gac gtc gat ttc acc  
 355 Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr  
 70 75 80  
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 403 Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly  
 90 95 100  
 atc atc ttc tcc gtt ctt gtt ttc ttg gga ctg act cgc cct cgc gtc  
 451 Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val  
 105 110 115  
 cgt gcc aac gaa gac ggc gtt gag gtc ggt gag gtc cgt aac ttc atc gga act cgt  
 499 Arg Ala Asn Gln Asp Gly Val Gln Val Arg Asn Phe Ile Gly Thr Arg  
 120 125 130  
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 Val Asp Ile Trp Ser 1  
 gga cta gac agc gtc ccg gct gat ctt caa gga tca gta gtc acc att 163  
 Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile 20  
 ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211  
 gtt gtt ttt gat ggc ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt 30  
 Ala Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys 35  
 ggc aag aag aag aag aag aag aag aag aag aag aag aag aag aag aag 40  
 Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Gln Pro Thr 45  
 cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct ggc gaa tgt ggc 55  
 Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Gln Cys Gly 60  
 gtc gat gct ggc ttg gtt att gat ttc act aaa gaa ctc gca ggt ctc 65  
 Val Asp Ala Ala Leu Val Ile Asp Thr Leu His Ala 70  
 Val Asp Ala Ala Leu Val Ile Asp Thr Leu His Ala 75  
 Val Asp Ala Ala Leu Val Ile Asp Thr Leu His Ala 80  
 Val Asp Ala Ala Leu Val Ile Asp Thr Leu His Ala 85  
 gtc gat gct ggc ttg gtt att gat ttc act aaa gaa ctc gca ggt ctc 90  
 Val Asp Ala Ala Leu Val Ile Asp Thr Leu Asn Leu Ala Gly Leu 95  
 Ser Ala Gln Gln Tyr Phe Thr Met Ile Val Asp Thr Leu His Ala 100  
 agc gct gaa gaa gat tat ttc aca acc atg atc gtc gat agc ctc gat 105  
 Ser Ala Gln Gln Tyr Phe Thr Met Ile Val Asp Thr Leu His Ala 110  
 cgt tca gtt gtc gtc ggc gag aac ttc acc ttc ggt gtc aat ggc gct 115  
 Arg Ser Val Val Val Gly Gln Phe Thr Val Asn Gly Ala 120  
 ggc act gag tcc acc atg cgg gaa ttg gga caa aag ttc ggc gtc aat 125  
 Gly Thr Gln Ser Thr Met Arg Gln Leu Gly Gln Lys Phe Gly Val Asn 130  
 gtc acg att gct ccg ctc ctc gat gat gat gat gac cag cgt att tgc tcc 135  
 Val Thr Ile Ala Pro Leu His Asp Asp Asp Asp Asp Asp Asp Asp 140  
 gtc acg att gct ccg ctc ctc gat gat gat gat gac cag cgt att tgc tcc 145  
 Val Thr Ile Ala Pro Leu His Asp Asp Asp Asp Asp Asp Asp Asp 150  
 acc ttg gtc gtc cgc gat tac ttg gat cag ggc gag gtt gag cgc gac aac 155  
 Thr Leu Val Arg Asp Tyr Leu Asp 160  
 acc ttg gtc gtc cgc gat tac ttg gat cag ggc gag gtt gag cgc gac aac 165  
 Thr Leu Val Arg Asp Tyr Leu Asp 170  
 acc ttg gtc gtc cgc gat tac ttg gat cag ggc gag gtt gag cgc gac aac 175  
 Thr Leu Val Arg Asp Tyr Leu Asp 180

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Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys 85  
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Glu Leu Ala Ala Gly Leu Ser Ala Glu Tyr Phe Thr Met Ile Val 100  
105 110

Asp Thr Leu His Ala Arg Ser Val Val Gly Glu Asn Phe Thr Phe 115  
120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln 130  
135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp 145  
150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Gln 165  
170 175

Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly 180  
185 190

Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro 195  
200 205

Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly 210  
215 220

Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys 225  
230 235 240

Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr 245  
250 255

Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg 260  
265 270

Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly 275  
280 285

His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys 290  
295 300

Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr 305  
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Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp 325  
330 335

Thr Gln Pro Ser Ala 340

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<212> DNA

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<223> RXA02135

<400> 571

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115 Met Val Pro Ala Gln

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc atc ctg gct cag acg  
163 Leu Phe Ala Arg Val Gln Phe Pro Asp His Lys Ile Leu Ala Gln Thr

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag  
211 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gln Ser Leu Gln Lys

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg  
259 Leu Gln Gln Ile Gln Ile Gln Cys Gln Gln Ile Pro

cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac  
307 Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gln Asp His

ggc gtt gca act aaa ggc gtg tcc ggc tac cca tcc tca gta agc ttg  
355 Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu

cag atg gct gaa aac att aca aac ggt ggc ggc ggc atc aac gta att  
403 Gln Met Ala Gln Asn Ile Thr Asn Gly Ala Ile Asn Val Ile

gca cgc acc acc ggc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac  
451 Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc  
499 His Gln Ala Trp Gly Asp Gln Arg Val Ser Arg Ser Cys Gly Ser Ile

gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag  
547 Asp Val Gln Asp Ala Met Thr Gln Gln Val Gln Arg Ala Leu Lys

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc ggc gac att  
595 Ile Gly Lys Arg Ile Ala Asp Gln Gln Val Asp Ala Gly Ala Asp Ile

tta atc ccc ggc gat tta gga att ggc aac acc acc acc acc gct ggc  
643 Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc  
691 Leu Val Gly Thr Phe Thr Leu Ala Gln Pro Val Val Val Val Gly Arg

ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc 739

1197	gag taactttcta agcgatgtcc ggc	Gln
1171	gta gtc gat gga ccc cta aac ggc tct tcc gaa gcg ccc gag caa aac acg	Val Asp Gly Pro Leu Asn Ala Ser Ser Gln Ala Pro Gln Asn Thr
1123	att gcc gtt gac ctg aac gac atg tgc aca ttt tct tcc gcc ggc	Ile Ala Val Asp Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
1075	tcc ctt gcc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag	Ser Leu Gly Gln Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
1027	gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg	Val Ala Leu Asn Ala Leu Ala Leu Ile Leu Gln Leu Gly Met
979	agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Gln Pro Ala His Ser
931	gta gtc acc gcc gca gcc ctc cta gcc aac aaa cta ggc cca ggt gcc	Val Val Thr Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala
883	att gcc caa gca gca gtc cga cgc acc ccc gtg ctt ctc gac ggc gtt	Ile Ala Gln Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val
835	atc gcc cgg aaa atc tct tcc cca gac ctt gca ggc atg gca gca ttc	Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Met Ala Ala Phe
787	cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala
	Gly Thr Gly Ile Asp Asp Gln Ala Trp Lys Leu Lys Val Ser Ala Ile	200 205 210
	Met Val Pro Ala Gln Leu Phe Ala Arg Val Gln Phe Pro Asp His Lys	1 5 10 15
	Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro	20 25 30
	Gly Ser Leu Gly Lys Leu Gln Ile Gly Cys Phe Ile Ser Ala Cys	35 40 45
	Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val	50 55 60

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<400> 572

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90

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile 100  
105 110

Asp Thr Ser Ser Leu Asp His Gln Ala Trp Gly Asp Gln Arg Val Ser Arg 115  
120 125

Ser Cys Gly Ser Ile Asp Val Gln Asp Ala Met Thr Gln Gln Val 130  
135 140

Gln Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Gln Val Asp 145  
150 155 160

Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr 165  
170 175

Thr Thr Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Gln Pro Val 180  
185 190

Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Gln Ala Trp Lys Leu 195  
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Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg 210  
215 220

Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala 225  
230 235 240

Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val 245  
250 255

Leu Leu Asp Gly Val Val Val Thr Ala Ala Leu Leu Ala Asn Lys 260  
265 270

Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr 275  
280 285

Gln Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile 290  
295 300

Leu Gln Leu Gly Met Ser Leu Gly Gln Gly Ser Gly Ala Ala Thr Ala 305  
310 315 320

Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr 325  
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>222> (101)..(1123)
>223> RXA01489
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Val Asp Ile Trp Ser 1  
5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163  
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile 20

211 ggt gtc ttc gat ggc ctc cac cgg ggc cat caa agt tta atc ggc gag  
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Gln

gcc aag aag cag gcc gag gag cag cgt ggt gtc atg cct gtc atg Met Val Thr  
Ala Lys Lys Gln Ala Gln Gln Gln Leu Gln Gly Val Pro Cys Val Met Val Thr  
40  
45  
50  
259

307 ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc  
phe asp pro his pro ile ala val phe leu pro gly lys glu pro thr

355	cgt	ttg	gct	cct	ttg	gat	tat	cgc	ctt	aat	ttg	gct	gcg	gaa	tgt	ggc
	Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	Ala	Ala	Gln	Cys	Gly
	70					75					80					85

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Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu 100

451 agc gct gaa gag tat ttc acc acc atg atc gtc gat acg ctg cat gcg  
Ser Ala Gln Gln Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala

499	cgt tca gct	120	arg ser val
	gct gct gct		val val val
	gag gag gln	125	asn asn
	aac ttc acc		phe phe phe
	acc ttc ggc		thr thr thr
	gct gct gct	130	gly gly gly
	gct gct gct		val val val
	aat ggc ggc		asn asn ala
	gct ggc ala		

	ggc	act	gag	tcc	acg	atg	met	arg	cgg	gga	ctg	gga	caa	agg	ctt	ggc	gtg	aat	54 /
	Gly	Thr	Glu	Ser	Thr	Met	Arg	Gln	Glu	Leu	Gly	Gln	Lys	Phe	Gly	Val	Asn		
	135								140					145					

[illegible]

	Thr	Leu	Val	Arg	Asp	Tyr	Leu	ASP	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn	643
	acc	ctg	gtc	cgc	gat	tac	ctg	gat	cag	ggc	gag	gtt	gag	cgc	cgc	aac	
	170									175						180	

691 Trp Ala Leu Gly Arg Arg Arg Tyr Ala Val Arg Gly Gln Val Val Arg Gly

185	190	195
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcc aat ctc tac	Ala Gly Arg Gly Gly Lys Gln Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	Phe Thr Ile Thr Asp Asp Arg Gln Ile Asp Lys Gln Ile Ser Arg Asp	835
atc gac ggc acc atg gtc cca ggc gtc gtc cgt tac caa act gcc att tcc	Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser	883
gtg ggc acc aat ccc acc ttc ggc gat gac gac arg gca ggc gat gca	Val Gly Thr Asn Pro Thr Phe Gly Asp Gln Arg Arg Ser Val Gln Ala	931
ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg	Phe Ile Leu Asp Gln Gln Ala Asp Leu Tyr Gly His Val Met Val	979
gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac	Gln Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp	1027
gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc	Gln Leu Leu Asp Ala Met Ala Arg Asp Ile	1075
ctt gcc aaa gac aaa ttg ctc gac gcc gac acc cag ccc agc gct	Leu Ala Lys Asp Lys Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala	1123
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1146		
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Ser Leu Ile Gly Gln Ala Lys Lys Gln Ala Gln Gln Leu Gly Val Pro	35	
Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro	50	
Gly Lys Gln Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu	65	

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Met Ile Val 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln 130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp 145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly 165 170 175

Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly 180 185 190

Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro 195 200 205

Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly 210 215 220

Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys 225 230 235 240

Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr 245 250 255

Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg 260 265 270

Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly 275 280 285

His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys 290 295 300

Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr 305 310 315 320

Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp 325 330 335

Thr Gln Pro Ser Ala 340

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<222> (87) .. (782)

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Met Val Asp Ile Leu Gln Ile Gly  
1

ccc cta cct ttc gtg tct acg cca gag tta agg gca atc gtc gtg act  
Pro Leu Pro Phe Val Ser Thr Pro Gln Leu Arg Ala Ile Val Val Thr  
10 20 25

gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga  
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly  
30 35 40

aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tgg gac  
Asn Ser Thr Asp Thr Gln Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp  
45 50 55

gtg gtg ttg ttg gtt ggt tgg acg agc agc gtg aag gct gaa aat tat ggt ggc  
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Gln Asn Tyr Gly Gly  
60 65 70

gtg gag ggt ttg tgg cct gaa atc cag aag caa cgc cag gag ttg ggt cag  
Val Gln Val Ser Pro Gln Ile Gln Lys Gln Arg Gln Gln Leu Gly Gln  
75 80 85

gaa gcg att cgc cgc att gcg gtg atg tca ggg tgg ttg aat ttt gat  
Gln Ala Ile Pro Pro Ile Ala Val Met Ser Ser Gly Ser Leu Asn Phe Asp  
90 95 100 105

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Val Asp Thr Arg Phe Phe Leu Gln Ala Gln Val Pro Pro Ile Ile Ile  
110 115 120

acg gat aat tcc gat caa gca aag cag cag cag cgt ctt gtt gat gct ggg  
Thr Asp Asn Ser Asp Gln Ala Lys Gln Arg Leu Val Asp Ala Gly  
125 130 135

gct cag gtt att gag gtg gag acg ttg acg gcg gag ggt ggc gtc gaa  
Ala Gln Val Ile Gln Val Gln Thr Leu Thr Ala Gln Val Gly Val Gln  
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Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Gln Gly Gly Ala  
155 160 165

acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtt gtt cat  
Thr Leu Tyr Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His  
170 175 180 185

cac acg att gat cgc acg ttg tgg agc ttg gag cgc ccc acg gtt  
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Gln Arg Pro Thr Val  
190 195 200

aag ggc ggc gat gat ggc cgc cgc cgc cga ttc gcg ttg gag cac gtc ttt  
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Gln His Val Phe  
205 210 215

gtc gat gat gac agc acc cta ttc ctg cgg tat aag cgc gcc aag  
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<213> Corynebacterium glutamicum

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Ile Asn Gly Thr Ser Gly Glu Leu Gly Asn Ser Thr Asp Thr Glu Leu  
35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
85 90 95

Val Met Ser Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Leu  
100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu  
210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys  
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<223> FRXA01712

<400> 577

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105 Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys  
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caa cgc cag gag ttg ggt cag gaa ggc atc cgc cgc att ggc gtg atg  
153 Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met  
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tca ggg tcg ttg aat ttg gat gtg gat act cgc ttg phe Leu Glu Ala  
201 Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala  
35 40 45

gaa gtg cgc cgc cgc atc atc atc acg gat aat tcc gat caa gca aag cag  
249 Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln  
50 55 60

cag cgc ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg  
297 Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu  
70 75 80

acg ggc gag gtt ggc gtc gaa aag ctt agt tct ttg ggt tac ggc cgc  
345 Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg  
85 90 95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg ggc ggc  
393 Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala  
100 105 110

gat ctt gtt gat gtt ggt tgg cat cac acg att gat cag acg ttg tcg ggc  
441 Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly  
115 120 125

acg gtg gag cgc ccc acg gtg aag ggc ggc gat gat ggc cgc cgc cga  
489 Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg  
130 135 140 145

ttc ggc ttg gag cac gtc ttc gtc gat gat gac agc acc cta ttc ttg  
537 Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu Phe Leu  
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578 Arg Tyr Lys Arg Ala Lys  
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<211> 167  
<212> PRT

<213> Corynebacterium glutamicum  
 <400> 578  
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 Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu  
 35 40 45  
 Ala Glu Val Pro Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys  
 50 55 60  
 Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr  
 65 70 75 80  
 Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
 85 90 95  
 Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala  
 100 105 110  
 Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
 115 120 125  
 Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
 130 135 140  
 Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu Phe  
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 Leu Arg Tyr Lys Arg Ala Lys  
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 Val Thr Arg Arg Leu  
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 att ctg ctc cga cac ggg cag act gaa tac aac gcc acc gcc acg tcc cga atg 163  
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met  
 10 15 20  
 cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttc caa cag gcg 211  
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Ala  
 25 30 35

gac agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259  
Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe 40  
agg tgc gat ctt tcc cgc gcc ttc aac acc gca agc gca ggt gtc ggc 55  
Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala 65  
ctg att gac gcg gag gtg cgc gat aag cgt ctt cgg gaa acc cat 355  
Leu Ile Asp Ala Gln Val Arg Val Asp Lys Arg Leu Arg Gln Thr His 85  
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat 403  
Leu Gln Asp Lys Thr His Thr Gln Val Asp Ser Gln Tyr 100  
cca ggt gcg cgc gct caa tgg cgc gat cag tgg gca cca ccc 451  
Pro Gln Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro 115  
ggc ggc gaa tgc cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc 499  
Gly Gly Gln Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val 120  
gac gag tgg atg gtg tgc ctt gat gat tgg gat gaa ggc acc gtg ctc 547  
Asp Gln Leu Met Val Ser Leu Asp Asp Trp Asp Gln Gly Thr Val Leu 135  
atc gtg gct cac ggt ggc agc att aat gcg ctg acc tgc aat ctt ttg 595  
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu 150  
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc 643  
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr 170  
tgt tgg gca caa tgg acc gcc cga cct cgc tat tat gca ggt agt gag 691  
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Gln 185  
aac cca gaa gat gac ctc aag att tct tgc gcg ggt tcc aac agc cct 739  
Asn Pro Gln Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro 200  
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc 787  
His Phe Gln Gly Asn Asn Val Gln Asn Ala Gln Trp Tyr Leu Asp Gly 215  
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg 831  
Trp Asn Met Gly Val Thr Gln 235

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<211> 236  
<212> PRT  
<213> Corynebacterium glutamicum  
<400> 580  
Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Gln Tyr Asn



1 5 10 15

Ala Thr Ser Arg Met Gln Gln Gly Thr Gln Leu Ser Asp Leu 20 25 30

Gly Phe Gln Gln Ala Ser Ala Ser Val Leu Val Gln Lys Asn 35 40 45

Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala 50 55 60

Ser Ala Val Ala Ala Leu Ile Asp Ala Gln Val Arg Val Asp Lys Arg 65 70 75 80

Leu Arg Gln Thr His Leu Gly Gln Trp Gln Ala Lys Thr His Thr Gln 85 90 95

Val Asp Ser Ser Gln Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro 100 105 110

Gln Trp Ala Pro Pro Gly Gln Ser Arg Val Asp Val Ala Arg Arg 115 120 125

Ala Arg Gln Val Val Asp Gln Leu Met Val Ser Leu Asp Asp Trp Asp 130 135 140

Gln Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu 145 150 155 160

Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser 165 170 175

Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr 180 185 190

Tyr Ala Gly Ser Gln Asn Pro Gln Asp Asp Leu Lys Ile Ser Ser Ala 195 200 205

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Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln 225 230 235

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<211> 453

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN01560

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Val Gly Val Ser Tyr 5

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211	att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga	Ile Gly Gln Thr Phe Lys Thr Gln Ile Ile Leu Gly Gly Gly	35
259	acc ctg aac tgg tcc atg ctg cgc gac ggt ttg tgc gag ggt agc	Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Gln Val Ser	40
307	atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg	Ile Val Met Met Pro Ile Ala Asp Gly Gln Lys His Thr His Ser Leu	55
355	ttc gaa gcc gat gaa aaa tac tca gca cgc ttg ccg atc ggt ttt tca	Phe Gln Ala Asp Gln Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser	70
403	ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac	Leu Ala Ser Val Gln Pro Leu Gln Asp Gly Ser Val Trp Met Arg Tyr	90
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453	ttt		
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<213> Corynebacterium glutamicum			
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55	Cys Asp Gln Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Gln Lys		55
60			60
65	His Thr His Ser Leu Phe Gln Ala Asp Gln Lys Tyr Ser Ala Pro Leu		65
70			70
85	Pro Ile Gly Phe Ser Leu Ala Ser Val Gln Pro Leu Gln Asp Gly Ser		85
90			90
100	Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn		100
110			110

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				Met Ile Ala Leu Lys		
				1		5

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Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp

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cag cgc cac cgc atc ccg gcc gac aac gcc gaa gga gln ala arg  
gln arg his arg asn pro ala asp asn ala gln ala leu gln ala arg

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cag cgc cac cgc atc ccg gcc gac aac gcc gaa gga gln ala arg

65  
cag cgc cac cgc atc ccg gcc gac aac gcc gaa gga gln ala leu gln ala arg

gac acc atg gtt cag gcc gac gac gac gac att tgg ttc tac cgc atg gcc  
asp thr met val gln pro asp asp asp asp ile trp phe tyr arg met pro

gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct  
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro

act gga aac aac gat ctc acc cca gat cac cgc ctc gat cgc ctc gat cgc ctc act  
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr

150 155 160 165

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739	gca gaa ttc gtc cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa Ala Gln Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Gln	200	205	210	787	tcc cgc atc gaa aaa gaa ggc ggc atc gtc gaa ggc ttc gtc gtc gaa Ser Arg Ile Gln Lys Gln Arg Gly Ile Val Gln Ala Phe Val Val Gln	215	220	225	835	ggc ccc gtc aac gca gca ggc act gaa ctg gtc tca gtc acc cca gtc gaa Gly Pro Val Asn Ala Arg Thr Gln Leu Val Ser Val Thr Pro Val Gln	230	235	240	245	883	gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc Asp Ala Gln Gln Ser Ile Leu Gln Gln Met His Gly Pro Leu Pro Arg	250	255	260	931	caa gcg cgc tac gtc cta gcc ccc tca aca ggc aaa acc cca cag ctg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu	265	270	275	979	cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac gcc ctc Arg Ile His Met Arg Asp Phe Ala Pro Ile Leu Gly Asp Pro Leu	280	285	290	1027	tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg Tyr Pro Val Leu His Ala Val Asp Asp Gln Asp Tyr Thr Thr Pro Met	295	300	305	1075	cac ctc atc gcc cgc acg cta acc ttc gtc gat cct caa acc aac gag His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Gln	310	315	320	325	1124	gaa cgt acc ttt gtc agt aat cga cct acg gga agt ttg taggcctcgt Gln Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu	330	335	1137	agacatcaccc cag
-----	--	-----	-----	-----	-----	--	-----	-----	-----	-----	--	-----	-----	-----	-----	-----	--	-----	-----	-----	-----	--	-----	-----	-----	-----	--	-----	-----	-----	------	--	-----	-----	-----	------	--	-----	-----	-----	-----	------	---	-----	-----	------	-----------------

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Arg Leu Pro Leu Asp Ala Pro Ile Arg Ala Ile Asp Phe Val Gln  
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40  
55  
60  
Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Gln  
50  
Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly

65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Ile Trp 85 90 95

Phe Tyr Arg Met Pro Ala Ala Gln Arg Pro Ile Pro Tyr Lys Ile His 100 105 110

Val Ile His Gln Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr 115 120 125

Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Gln Thr Ala Leu Val 130 135 140

Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg 145 150 155 160

Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Gln 165 170 175

Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Gln Ala Ser Lys 180 185 190

Thr Tyr Gln Ala Ile Ala Gln Phe Val Pro Gly Leu Leu Asp Asp Gly 195 200 205

Pro Ala Ile Trp Gln Ser Arg Ile Gln Lys Gln Arg Gly Ile Val Gln 210 215 220

Ala Phe Val Val Gln Gly Pro Val Asn Ala Arg Thr Gln Leu Val Ser 225 230 235 240

Val Thr Pro Val Gln Asp Ala Gln Ser Ile Leu Gln Gln Met His 245 250 255

Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly 260 265 270

Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Pro Ile 275 280 285

Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Gln Asp 290 295 300

Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp 305 310 315 320

Pro Gln Thr Asn Gln Gln Arg Thr Phe Val Ser Asn Arg Pro Thr Gly 325 330 335

Ser Leu

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Met Leu Met Ala 1

cat cgc ttc ttc tgc ctt ggc att aac ggc gca gtc acc gac gat ttc  
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Phe 20

acg acg gtc tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc  
Thr Thr Val Tyr Ser Ala Leu Arg Phe Val Glu Gly Ile Pro Val 35

tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg  
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro 50

ggc gcc acc ctc cta tgc gca cca tgc gga tat atc acc cat ttc acg  
Gly Ala Thr Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr 65

ttg gct cgc tgc atg ttc atc ggc gtc aac ctc ctc gcc att gtt tta  
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu 85

ggc ttc tgc ggc cgc cgc cgc acc aga ctc tcc ggt tgc ggc cgc agc atg  
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met 100

gtg tgc cgc att ggc atc gcc tgc ggc atg cgc atg cta gaa acc gtc caa  
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Glu 115

aac acc ctc att ttc tcc aac atc aac ggc atc ctc cgc ctc atg tgc  
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Met Leu 130

ggc att ttc cgc tgc tgc gtc gtc cac aaa aaa tcc tgc tgc ggc gga  
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly 145

cta gtc att ggt tgc gcc att tgc atc aaa ccc atg ttc cgc cca ctt  
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu 165

ctc ttc cta cta cct tgc gtc gtc aaa aag caa tgc gga tgc ggc tgc atc ctc ggc  
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly 180

att tta acc cca gtc att ttc aat gca gtc gcc tgc tgc ttc tta gtc ccg  
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro 195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctc ggt gaa act  
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Thr 210

787 cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga  
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 Met Pro Thr Trp Met Gln Ile Thr Trp Phe Leu Ile Phe Gly Ala Met  
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 265 270 275  
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 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile  
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 360 365 370  
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 Gln Gly Ile Pro Val Tyr Asn Gln Val Tyr His Phe Val Asp Pro His  
 30

BGI-121CP

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Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr	50	60
Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu	65	75
Leu Ala Ile Val Leu Ala Phe Gly Leu Leu, Thr Arg Leu Ser Gly Trp	85	90
Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu	100	110
Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile	115	125
Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys	130	140
Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro	145	155
Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly	165	170
Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala	180	185
Trp Phe Leu Val Pro Gly Ala Ser Gln Tyr Val Thr Arg Thr Met Pro	195	205
Tyr Leu Gly Gln Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu	210	220
Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Gln Ile Thr Trp Phe Leu	225	235
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe	245	255
Arg Asn Thr Gln Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu	260	270
Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser	275	285
Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val	290	300
Phe His Asn Trp Val Ala Trp Val Ala Tyr Phe Leu Leu Ser Pro	305	315
Asp Thr Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Gln	325	335
Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe	340	350
Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr	355	365



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380  
Thr Ala  
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385

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<212> DNA  
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115 Met Thr Thr Val  
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aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttg gac ccc att  
163 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
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cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat  
211 His Asn Gly His Leu Val Ala Gly Ser Gln Val Ala Asp Arg Phe Asp  
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ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg  
259 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala  
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aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc  
307 Asn Lys Lys Val Ser Pro Ala Gln Asp Arg Tyr Leu Met Thr Val Ile  
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gcc act gcc tct aat cca cga ttt atg gta tcg cgg gtt gat att gat  
355 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp  
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cgg gga ggg gat act tac acg atc gat acc ctg caa gat tgg agc aag  
403 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys  
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caa tac cag gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg  
451 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu  
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gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctg gcc  
499 Ala Gln Ile Val Thr Trp Arg Asp Trp Gln Lys Thr Phe Gln Leu Ala  
130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc  
547 His Phe Val Gly Val Thr Arg Pro Gly Tyr Gln Leu Asp Gly Asn Ile  
145

ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg  
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595	att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc	150	ile pro glu met his gln asp arg val ser leu val asp ile pro ala	165
643	atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc	170	met ala ile ser thr asp cys arg glu arg ser ser glu arg	180
691	cct gtt tgg tat ctt gtc cct gat ggc gtg cgt caa tac att gcc aaa	185	pro val trp tyr leu val pro asp gly val val gln tyr ile ala lys	195
739	cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag	200	arg gln leu tyr arg pro glu gly ser asp lys asp met asp pro lys	210
777	ggc caa aac caa gca taaatctagt caaaagtctc aac	215	gly gln asn gln ala	

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 Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
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 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Gln Asp Arg Tyr  
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 Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
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 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
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 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
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 110  
 Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Gln Lys  
 115  
 120  
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 Thr Phe Gln Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Gln  
 130  
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 140  
 Leu Asp Gly Asn Ile Ile Pro Gln Met His Gln Asp Arg Val Ser Leu  
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 Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Gln Arg  
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 170  
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 Ser Ser Gln Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

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 400  
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 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile 20  
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cat aat ggt cac ctt gtg gcg ggc tca gag gta gca gcg gat cga ttc gat  
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 Leu Asp Leu Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala 50  
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gca cag atc gtc acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc  
 Ala Gln Ile Val Thr Trp Arg Asp Trp Gln Lys Thr Phe Gln Leu Ala 130  
 499

cac ttc gtt gga gga gtc act cga ccc ggt tat gaa tgg gat gga aac atc  
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Gln Leu Asp Gly Asn Ile 145  
 547

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595	att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc	150	Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala	165
643	atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc	170	Met Ala Ile Ser Ser Thr Asp Cys Arg Gln Arg Ser Glu Arg	180
691	cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa	185	Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys	195
739	cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag	200	Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys	210
777	ggc caa aac caa gca taaatctagt caaaagtctc aac	215	Gly Gln Asn Gln Ala	
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50	Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr	55		60
65	Leu Met Thr Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser	70		75
80	Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu	85		90
100	Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr	105		110
115	Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys	120		125
130	Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu	135		140
145	Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu	150		155
165	Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg	165		170
175				175

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Ile Arg Asn Ile Asp Ser Ile Asp Gln Leu Pro Leu Pro Ala Gln

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Lys Ala Gly Phe Gln Pro Lys Arg Arg Gln Gly Asn Arg Gln Asn Arg
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70
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Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
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Ala Gln Arg Gln Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
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Ser Asp Gln Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Gln Leu Pro
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Pro Leu Pro Ala Gln Tyr Gln Pro Gly Tyr Gln Asp Asp
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1699	cct gtc cgc cca ccg atg tcc ggc ggt att gtc ggc gga cct cgc ctg	520	Pro Val Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu	530
1747	glt ccc ggc ggc cca gtc ggc gag ggt cgt ttc cgt ctg ctg ggc gat	535	Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Ala Asp	545
1795	cac ggc ggc gtc caa ggc cgt ttc tgg cag ggc cgc gag atc ggc	550	His Gly Gly Val Gln Gly Ala Arg Gln Ala Arg Gln Ile Ala	560
1843	acc ggc aag gaa gtc ggc ctg atc ttt gtc gat act tcc ggc aac ggc	570	Thr Gly Lys Gln Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala	580
1891	cca ttt gcg cca ctg tct tcc gca ggc gca ggc ggc ggc atc ggc tac	585	Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Gly Ile Ala Tyr Gln	595
1939	gtg cag cgc cgc acc aag aag ctg ggc agc tgg ggc agc tgg ggc gta	600	Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val	610
1987	gcc ccc aac atc cac tcc gag ggc tac cgc aac ggt tgc ctg att gtc	620	Ala Pro Asn Ile His Ser Gln Ala Tyr Arg Asn Gly Cys Leu Ile Val	625
2035	gcc gat tgg gtc cct ggc tcc agc tgg agc ggc gtc ggc gaa tcc ggt	635	Ala Asp Trp Val Pro Gly Ser Ser Ser Leu Ser Ala Val Ala Gln Ser Gly	645
2083	gcc gat ccc ggc ggc ggc ttc ggc ctg ggc ggc gaa cta act gaa acc	650	Ala Asp Pro Arg Ala Ala Phe Ala Leu Ala Gln Leu Thr Gln Thr	660
2131	atc ggc gag ggc cac gag atg ggt atc cgc ggc ggc gtc gtc gac aac	665	Ile Gly Gln Ala His Gln Met Gly Ile Pro Ala Gly Leu Asp Asn Lys	675
2179	tgc cga att cgt atc aac acc gag ggc cat ggc gtc gtc gtc gtc ccg	680	Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro	690
2227	gcg att ttg ccc gat gcc tca gag ctg cgc gag ggc aag tcc ctg ggc	695	Ala Ile Leu Pro Asp Ala Ser Gln Leu Arg Asp Ala Lys Ser Leu Ala	705
2275	tcg gcc gcc gag atg ctt atc gag ggc acc ctc gct gcc agc gag gtc	715	Ser Ala Ala Gln Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val	725
2323	aag gca atg gtc act gaa gcc cag ggc cta gct aca gaa gag aat ccc	730	Lys Ala Met Val Thr Gln Ala Gln Gly Leu Ala Thr Gln Asp Asn Pro	740

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 1699  
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 2323

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2419	gag gaa cca acc cac cta gta gta gta gta gta gta gta gta gta	Glu Gln Pro Thr His Leu Val Lys Lys Lys Lys Lys Lys Lys	760	765	770
2467	gcg aca cgt gat ggt ttc ggt ggc tcc gac tac acc gtc aag ggc atg	Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met	775	780	785
2515	gca gcc atc gcc gct gta gta gta gta gta gta gta gta gta gta	Ala Ala Ile Ala Val Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile	790	795	800
2563	ggt acc gcc ttc cta acc agc ttc ttc ggc agc agc acc aac gaa caa	Gly Thr Ala Phe Leu Thr Ser Phe Gly Ser Ser Ser Thr Asn Gln Gln	805	810	815
2611	tcc ccg ttc ggc tct gta gaa gcc acc acc acc tct gca aca cca gaa cct	Ser Pro Leu Ala Ser Val Gln Ala Thr Ser Ala Thr Pro Gln Pro	820	825	830
2659	gtg ggc cca ccg gtc tac gta gta gta gta gta gta gta gta gta	Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp	835	840	845
2707	gac ggt gca gga gca gta gta gta gta gta gta gta gta gta gta	Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser	850	855	860
2755	acc gca tga acc tcc acc gcc gcc gcc gcc gcc gcc gcc gcc gcc	Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser	865	870	875
2803	acg cct gcc ccg ctc gcc gac gcc gac gcc gac gcc gac gcc gac	Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser	880	885	890
2851	gac agc aac gta acc tgc acc tgc acc gta acc gta acc gta acc gta	Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala	895	900	905
2899	tca cca cac tcc ccg tgc gaa ggc atc gag atc ggc acc gtc gat tat	Ser Pro His Ser Leu Ser Gln Gly Ile Gln Ile Gly Thr Val Asp Tyr	910	915	920
2947	tcc ggc ccg agt ctc acc cac agc atc cgc gat tcc tcc aag ctc ccg	Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro	925	930	935
2995	ggt cag gta gaa tcc gta gta gta gta gta gta gta gta gta gta	Gly Gln Val Gln Ser Val Ser Val Ile Leu Val Asp Gln Val Arg Ser Ser	940	945	950
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Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
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Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Glu  
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Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Glu  
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Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
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Arg Glu Val Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Val  
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His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
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Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
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Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
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Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
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Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
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Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
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100 200 300 400 500 600 700 800 900 1000

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Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser 335  
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Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala 575  
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Gly Ile Ala Tyr Gln Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Gln Ala Tyr Arg Asn  
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 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
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 Val Ala Gln Ser Gly Ala Asp Pro Arg Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Gln Leu Thr Gln Thr Ile Gly Gln Ala His Gln Met Gly Ile Pro Ala  
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 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
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 Ser Thr Asn Gln Ser Pro Leu Ala Ser Val Gln Ala Thr Thr Ser  
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 Ala Thr Pro Gln Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln  
 835 840 845  
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr  
 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
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 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Gln Gly Ile Gln Ile

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 Ser Ser Lys Leu Pro Gly Gln Val Gln Ser Val Ile Leu Val Asp  
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 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala 130  
 Asp Gln Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr 145  
 Gly Ile Ile Pro Asn Ala Phe Gln Leu Ser His Met Val Gly Ser Gly 165  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Gln Trp Ile Ile Thr 180  
 Ser Ala Thr Gln Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg 195  
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 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctc act gat aaa tat 163  
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 Gln Leu Thr Met Leu Gln Ala Leu Ala Asp Gly Ser Ala Gln Arg 35



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	Pro Ser Thr	phe glu val	phe ser arg	arg arg	leu pro	asn glu	arg arg		
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	Tyr Gly Val	val ala	thr ala	thr ala	arg val	leu lys	ala ile	arg asp	
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	phe val phe	thr glu	glu ala	leu ala	asp leu	asp phe	leu asp	asp	
403	cgt acc ctg	gaa tac	ctc cgc	aac tac	cga ttc	acc ggc	caa gtt	gat	100
	arg thr leu	glu tyr	leu arg	asn tyr	arg phe	thr gly	glu val	asp	
451	ggc tac cgc	gaa ggc	gaa att	tac ttc	cgc cag	tcc cct	ctt ctg	act	115
	gly tyr arg	glu glu	ile tyr	phe pro	glu ser	pro leu	leu thr		
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	val arg gly	thr phe	ala glu	cys val	ile leu	glu thr	val ile	leu	
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	ser ile met	asn ala	asp ser	ala val	ala ser	ala ala	ala arg	met	
595	gtc acc gca	gct gat	ggt cgc	ccc att	atc gaa	atg gga	tcc agg	cgc	145
	val thr ala	ala asp	gly arg	pro ile	ile glu	met gly	ser arg	arg	
643	acc cac gaa	tac tgc	gca gtc	acc gca	tcc cgc	gca gca	tac ctc	gct	155
	thr his glu	tyr ser	ala val	thr ala	ser arg	ala ala	tyr leu	ala	
691	gga ttc tcc	acc thr	tcc aac	ctc gag	gag gcc	tac gcc	tac gga	att	165
	gly phe ser	thr thr	ser asn	leu glu	ala ala	tyr arg	tyr gly	ile	
739	cca gca tcc	gga acc	tcc gcc	cac gca	tgc act	ttg ctg	cac atc	aac	175
	pro ala ser	gly thr	ser ala	his ala	trp thr	leu leu	his ile	asn	
787	gat gac ggc	acc ccc	aac gaa	gca gca	gct ttc	aaa gca	cag gtt	gaa	185
	asp asp gly	thr pro	asn glu	ala ala	ala phe	lys ala	glu val	glu	
835	tcc ctg ggc	gtg gac	acc acc	acc tgc	gtg gta	gat act	tat gac	atc	195
	ser leu gly	val asp	thr thr	leu leu	val asp	thr thr	tyr asp	ile thr	
883	caa ggt gtc	gcc acc	gcc att	gaa gtt	gca ggt	cca gac	ctt ggt	ggc	205
	glu gly val	ala thr	ala ile	glu val	ala gly	pro asp	leu gly	gly	
931	gta cgt atc	gac tcc	ggc gac	cta ggt	gtg gtt	gcc cga	aag gtc	cgc	215
	val arg ile	asp ser	gly asp	leu asp	val leu	ala arg	lys val	arg	





Gln Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys 370  
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 Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile 385  
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 Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys 405  
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 Val Asn Thr Asn Pro 1  
 163 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat  
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 211 gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc  
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 307 tac ggt gtc gtc gca gga aca gca cga gtc ctg aag gcg att cgt gac  
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 355 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac  
 Phe Val Phe Thr Glu Gln Ala Asp Leu Asp Phe Leu Asp Asp 85  
 403 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat  
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp 100  
 451 ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctg act  
 Gly Tyr Arg Glu Gly 105  
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499	gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ctg	Val Arg Gly Thr Phe Ala Gln Cys Val Ile Leu Gln Thr Val Ile Leu	120	125	130
547	tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Arg Met	135	140	145
595	gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Gln Met Gly Ser Arg Arg	150	155	160
643	acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	Thr His Gln Tyr Ser Ala Val Thr Ala Ser Arg Ala Tyr Leu Ala	170	175	180
691	gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	Gly Phe Ser Thr Ser Asn Leu Gln Ala Ala Tyr Arg Tyr Gly Ile	185	190	195
739	cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu His Ile Asn	200	205	210
787	gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtc gaa	Asp Asp Gly Thr Pro Asn Gln Ala Ala Phe Lys Ala Gln Val Gln	215	220	225
835	tcc ctc ggc gtc gac acc acc ttg ctg gta gat act tat gac atc acc	Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	230	235	240
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35	Gly Ser Ala Gln Arg Pro Ser Thr Phe Gln Val Phe Ser Arg Arg Leu		35	40	45
50	Pro Asn Gln Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu		50	55	60
65	Lys Ala Ile Arg Asp Phe Val Phe Thr Gln Gln Leu Ala Asp Leu		65	70	75
85	Asp Phe Leu Asp Asp Arg Thr Leu Gln Tyr Leu Arg Asn Tyr Arg Phe		85	90	95

Thr Gly Gln Val Asp Gly Tyr Arg Gln Ile Tyr Phe Pro Gln  
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 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Gln Cys Val Ile Leu  
 115 120 125  
 Gln Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Gln  
 145 150 155  
 Met Gly Ser Arg Arg Thr His Gln Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
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 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Gln Ala Ala Phe  
 210 215 220  
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 50 55 60  
 Ile Gly Gln Val Ala Gly His Pro Val Ala Lys Ser Arg Asn Lys  
 192

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240	gaa agc tac ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc	65	Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser	80
288	ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca	95	Gly Thr Ala Ile Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro	95
336	gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc	100	Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg	110
384	gac ggt gaa atc gtc cca ggt ttg cct act ttg gaa gat tcc cga gcg	115	Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala	125
432	tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg	130	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	140
480	tct cgc gat gag cct gtc ttg cac act cgt ttc gtg ggt ttc cgc ccg	145	Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro	160
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50	Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys	55		60
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100	Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg	105		110
115	Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala	120		125
130	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	135		140
135	Tyr Leu Ala Lys Glu Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu	140		145

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Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys  
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40 45 50

gcc tcc ttc cgg ctg gtc gat cct agt ata aac gca tcc ctt aag gtg 307  
Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val  
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gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355  
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Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly  
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 Ser Cys Tyr Val Ala Gln Val Lys Gly Thr Lys Ala Arg Ile Val Asp 115  
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Gln Arg Gln Ala Val 130  
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 Ile Thr Gln Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr 180  
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	Arg Pro Gln	Ala Ala	Gln Ile	Val Phe	Cys Gly	Val His	Phe Met	Ala	
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	Asp Gln His	Leu Gly	Arg Asn	Thr Ala	Lys Met	Gly Ile	Gly Ile		
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	Asp Gln Met	Pro Leu	Trp Asn	Pro Asn	Lys Pro	Leu Gly	Gly Asn	Thr	
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Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp	85	90	95
Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala	100	105	110
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 Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe 165  
 Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg 180  
 Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp 195  
 Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro 210  
 Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu 225  
 Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His 245  
 Leu Trp Lys Val Gly Gln His Lys Arg His Leu Pro Ala Thr Pro Gln 260  
 Glu Asn Trp Trp Arg 275

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[illegible]

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Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly  
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Gly Thr Lys Leu Gln Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val  
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 Arg Ile Phe Asp Gln Ala Gly Val Asp Met Leu Val Gly Asp Ser  
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 Ala Leu Val Val Val Val Val Val Val Val Val Val Val Val Val Val  
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Arg Gln Thr Gly Ala Ala Val Lys Ile Gln Gly Val Gln Ile 115  
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 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly 130  
 135  
 His Ile Gly Tyr Thr Pro Gln Ser Gln His Ser Leu Gly Gly His Val 145  
 150 155  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165  
 170 175  
 Ala Leu Gln Gln Ala Gly Ala Phe Ala Val Val Leu Gln Met Val Pro 180  
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 Ala Gln Ala Ala Arg Gln Val Thr Gln Asp Leu Ser Ile Thr Ile 195  
 200 205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210  
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 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Gln 225  
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355	atg att gtg ctg ggc aag gcg gtg acg atc gct acg aag cgt gcg ctt	70	Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu	80	
403	gtg gtg gtt gat ctg cgc ttt ggt acc tat gag gtg agc cca aat cag	90	Val Val Val Val Asp Leu Pro Phe Gly Thr Tyr Gln Val Ser Pro Asn Gln	100	
451	gcg gtg gag tcc gcg atc cgc gtc atg cgt gaa acg ggt gcg gct gcg	105	Ala Val Gln Ser Ala Ile Arg Val Met Arg Gln Thr Gly Ala Ala Ala	115	
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547	gtt gat gct gga att cgc gtt gtc ggc cac atc ggg tac acc ccg cag	135	Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln	145	
595	tcc gag cat tcc ttg ggc ggc cac gtc gtt cag ggt cgt ggc gcg agt	150	Ser Gln His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser	160	
643	tct gga aag ctc atc ggc gat ggc ggc ggc ttg gag cag ggt ggc	170	Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Gln Ala Gly Ala	180	
691	ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca ggc gcg gag gtt	185	Phe Ala Val Val Leu Gln Met Val Pro Ala Gln Ala Ala Arg Gln Val	195	
739	acc gag gat ctt tcc atc acc act atc gga atc ggt ggc aat ggc	200	Thr Gln Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly	210	
787	aca gat ggg cag gtt ttg gtt ttg cag gat ggc ttg ggc ctc aac cgc	215	Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg	225	
835	ggc aag aag cca cgc ttg gtc cgc gag tac ggc acc ttg ggc gat tcc	230	Gly Lys Lys Pro Arg Phe Val Arg Gln Tyr Ala Thr Leu Gly Asp Ser	245	
883	ttg cac gac ggc gcg cag ggc tac atc ggc gat atc cac gcg ggt acc	250	Leu His Asp Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr	260	
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Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser

Ile Thr Leu Asp Asp Gln Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Gln

Val Ser Pro Asn Gln Ala Val Gln Ser Ala Ile Arg Val Met Arg Gln

Thr Gly Ala Ala Val Lys Ile Gln Gly Gly Val Gln Ile Ala Gln

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile

Gly Tyr Thr Pro Gln Ser Gln His Ser Leu Gly Gly His Val Val Gln

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu

Gln Gln Ala Gly Ala Phe Ala Val Val Leu Gln Met Val Pro Ala Gln

Ala Ala Arg Gln Val Thr Gln Asp Leu Ser Ile Thr Thr Ile Gly Ile

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Gln Tyr Ala

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp

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&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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BGI-121CP

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09 հանձնարարքները համապատասխանում են իրենց նշանակմանը և չեն պահանջում ավելի մեծ ծախսեր:

cgcaagatat tgaactgtgg gcaattcaga aggaagaccg ttg agt ttc acg cat 115

1 5

163 ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc

10	15	20
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211 agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga

25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259

40	55	50
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atc ccc ggt gccg gtg gtc gtc gtc gtc gcc tat gcc gcc gcc gcc gcc gat      307

55 60 65

355 cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat

70 75 80 85

403 ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc

100 95 90

cca aca ctt acc cca caa ggt gcy gaa gta acc aag gty ctg ggg ctg 451

105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499

Don't say	120
Don't say	125
Don't say	130

gaq ctg qtt cta qtc caq cqc qcc ctt aat qat ctg cat att cca 547

135	140	145
135	140	145

qta aaa ctg cat tct qtt cca acc atg cgc atg cca gat qqa cta gcc 595

150	155	160	165
TRA	TRA	TRA	TRA
BYs	BYs	BYs	BYs
Den	Den	Den	Den
HIS	HIS	HIS	HIS
SEL	SEL	SEL	SEL
VAL	VAL	VAL	VAL
FIO	FIO	FIO	FIO
THI	THI	THI	THI
VAL	VAL	VAL	VAL
WEL	WEL	WEL	WEL
FIO	FIO	FIO	FIO
ASP	ASP	ASP	ASP
GLY	GLY	GLY	GLY
Den	Den	Den	Den
WIA	WIA	WIA	WIA

att tcc ctg cgt aat att tca atg ccc gaa gac tcc cgc gaa acc gca 643

170 175 180

[illegible]

Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His  
185 190 195

739

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ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca
787 Gly Val Thr Pro Asp Tyr Val Gln Ile Arg Gly Leu Asp Leu Gly Pro
      215      220      225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc
835 Ala Pro Gln Ile Gly Asp Ala Arg Leu Phe Ala Ile Thr Leu Gly
      230      235      240      245
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc
883 Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe
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35      40      45
Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Ala Tyr Ala
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Gly Pro Gln Ser Asp His Ala Arg Leu Arg Gln Gln Leu Ile Asp Ala
65      70      75      80
Ile Phe Pro Phe Asn Pro Gln Thr Leu Trp Pro His Gly Ile Arg Val
85      90      95
Gln Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Gln Val Thr
100      105      110
Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
115      120      125
Gly Gln Lys Asp Tyr Gln Leu Val Val Leu Val Gln Arg Ala Leu Asn
130      135      140
Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
145      150      155      160
Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Gln Asp
165      170      175
Ser Arg Gln Thr Ala Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala
180      185      190
His Ser Ala Gln His Gly Ala Val Val Lys Gln Thr Val Thr Gln

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195 205 200  
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Leu Asp Leu Gly Pro Ala Pro Gln Ile Gly Asp Ala Arg Leu Phe Ala  
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Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
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cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
Arg Asp Ser Gly Val Gln Val Ile Gly Leu Arg Gln Gly Ser Lys  
40 45 50  
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Ser Ala Gln Lys Ala Lys Gln Ala Gly Phe Gln Val Lys Thr Thr Ala  
60 65  
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Gln Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
70 75 80 85  
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Ser Gln Ala Gln Ile Phe Thr Asn Asp Ile Gln Pro Asn Leu Asn Ala  
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Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
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atc aag cca gct gac gac atc atc gtc ggc atg gtt gcg cca aag ggc 499

Protein	Accession	Length	MD5	Sequence
Protein A	P00001	120	120	Protein A
Protein B	P00002	135	135	Protein B
Protein C	P00003	150	150	Protein C
Protein D	P00004	165	165	Protein D
Protein E	P00005	180	180	Protein E
Protein F	P00006	195	195	Protein F
Protein G	P00007	210	210	Protein G
Protein H	P00008	225	225	Protein H
Protein I	P00009	240	240	Protein I
Protein J	P00010	255	255	Protein J
Protein K	P00011	270	270	Protein K
Protein L	P00012	285	285	Protein L
Protein M	P00013	300	300	Protein M
Protein N	P00014	315	315	Protein N
Protein O	P00015	330	330	Protein O
Protein P	P00016	345	345	Protein P
Protein Q	P00017	360	360	Protein Q
Protein R	P00018	375	375	Protein R
Protein S	P00019	390	390	Protein S
Protein T	P00020	405	405	Protein T
Protein U	P00021	420	420	Protein U
Protein V	P00022	435	435	Protein V
Protein W	P00023	450	450	Protein W
Protein X	P00024	465	465	Protein X
Protein Y	P00025	480	480	Protein Y
Protein Z	P00026	495	495	Protein Z
Protein AA	P00027	510	510	Protein AA
Protein AB	P00028	525	525	Protein AB
Protein AC	P00029	540	540	Protein AC
Protein AD	P00030	555	555	Protein AD
Protein AE	P00031	570	570	Protein AE
Protein AF	P00032	585	585	Protein AF
Protein AG	P00033	600	600	Protein AG
Protein AH	P00034	615	615	Protein AH
Protein AI	P00035	630	630	Protein AI
Protein AJ	P00036	645	645	Protein AJ
Protein AK	P00037	660	660	Protein AK
Protein AL	P00038	675	675	Protein AL
Protein AM	P00039	690	690	Protein AM
Protein AN	P00040	705	705	Protein AN
Protein AO	P00041	720	720	Protein AO
Protein AP	P00042	735	735	Protein AP
Protein AQ	P00043	750	750	Protein AQ
Protein AR	P00044	765	765	Protein AR
Protein AS	P00045	780	780	Protein AS
Protein AT	P00046	795	795	Protein AT
Protein AU	P00047	810	810	Protein AU
Protein AV	P00048	825	825	Protein AV
Protein AW	P00049	840	840	Protein AW
Protein AX	P00050	855	855	Protein AX
Protein AY	P00051	870	870	Protein AY
Protein AZ	P00052	885	885	Protein AZ
Protein BA	P00053	900	900	Protein BA
Protein BB	P00054	915	915	Protein BB
Protein BC	P00055	930	930	Protein BC
Protein BD	P00056	945	945	Protein BD
Protein BE	P00057	960	960	Protein BE
Protein BF	P00058	975	975	Protein BF
Protein BG	P00059	990	990	Protein BG
Protein BH	P00060	1005	1005	Protein BH
Protein BI	P00061	1020	1020	Protein BI
Protein BJ	P00062	1035	1035	Protein BJ
Protein BK	P00063	1050	1050	Protein BK
Protein BL	P00064	1065	1065	Protein BL
Protein BM	P00065	1080	1080	Protein BM
Protein BN	P00066	1095	1095	Protein BN
Protein BO	P00067	1110	1110	Protein BO
Protein BP	P00068	1125	1125	Protein BP
Protein BQ	P00069	1140	1140	Protein BQ
Protein BR	P00070	1155	1155	Protein BR
Protein BS	P00071	1170	1170	Protein BS
Protein BT	P00072	1185	1185	Protein BT
Protein BU	P00073	1200	1200	Protein BU
Protein BV	P00074	1215	1215	Protein BV
Protein				



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Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu 50 55 60  
Val Lys Thr Thr Ala Glu Ala Ala Trp Ala Asp Val Ile Met Leu 65 70 75 80  
Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu 85 90 95  
Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn 100 105 110  
Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met 115 120 125  
Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp 130 135 140  
Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly 145 150 155 160  
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Ala Tyr Phe Glu Val Leu His Glu Lys Leu Ile Val Asp Leu Met 225 230 235 240  
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Met Ala Ile Gln Leu  
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 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gln Gly Arg Lys Val 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Gln Val Ile Gly Leu Arg Gln Gly Ser Lys 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307  
 Ser Ala Gln Lys Ala Lys Gln Ala Gly Phe Gln Val Lys Thr Thr Ala 65

gag gct gca gct tgg gct gag gtc atc atg ctc ctg gct cca gac acc 355  
 Gln Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Gln Ile Phe Thr Asn Asp Ile Gln Pro Asn Leu Asn Ala 100

ggc gag gca cga ctg ctg ttc gag cgc cag ggc ctg aac att cac ttc gag ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu 115

atc aag cca gct gag gac atc atc gtc ggc atg gtc ggc cca aag ggc 499  
 Ile Lys Pro Ala Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly 130

cca ggc cac ctg gtc cgc cgt cag ttc gtc gat ggc aag ggt gtc cct 547  
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gag ggt gca gct tgg gct gag gtc atc atg ctc ctg gct cca gac acc 355  
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556

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Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
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Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
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Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
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Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtc gcc ggc 163

Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly	10	15	20
gga atc gca gca gca tac aag gcg tgt cac atc gtg cgc ggc ttc aaa gaa	25	30	35
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Gln	40	45	50
gca ggc gat aat gat cgc ggt gtc cct acg gaa tcc ggc ttg aag ttc	55	60	65
Val Gly Lys Ala Thr Phe Gln Ala Leu Ser Gly Asn Pro Val Ser Thr	70	75	80
acg gtg ttc gat gcg gta val asp ser val gln his val lys val gly gln	85	90	95
gaa gct gat ttg atc ttg att gca ggc gca ggc gca ggc gca ggc gca ggc	100	105	110
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala	115	120	125
403	130	135	140
gta ggc aat gta gca acg ctg gca acg ctg agg cag cgg	145	150	155
Trp Phe Asn Pro Ala Thr Val Ala Thr Leu Arg Gln Arg	160	165	170
ggt att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat	175	180	185
Thr Gly Pro Gly Arg Leu Pro Asp Pro Gln Ile Val Asp Leu Ala	190	195	200
aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg	205	210	215
Lys Val Leu Ile Thr Ala Gly Thr His Gln His Ile Asp Pro Val	220	225	230
Arg Phe Ile Gly Asn Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	235	240	245
gaa atc gca gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat	250	255	260
Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn	265	270	275
gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtc gtc cgc gtc gtc	280	285	290
Ala Ala Gln Leu Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr Pro Thr	295	300	305
883	310	315	320

250	260	255	260
tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct	Ser Thr Gln Asp Met Phe Asp Ala Val Gln Gln Arg Ala Gly Gln Ser	931	
gat ttc atc gtc atg gcg gca gca gta gct gat ttc acc ggc gca tcg	Asp Phe Ile Val Met Ala Ala Val Ala Asp Phe Thr Pro Ala Ser	979	
cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca	Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Gln Asp Ala	1027	
ttg agc acc atc tcg ttg ttg gaa aac ccg gat atc ttg gct acc acg	Leu Ser Thr Ile Ser Leu Val Gln Asn Pro Asp Ile Leu Ala Thr Thr	1075	
gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtc	Val Lys Arg Arg Gln Ala Gly Gln Leu Asp Ser Asn Pro Val Ile Val	1123	
ggt ttt gct gcg gaa act gga gac gag cac acc acc ggc ttg gag tat	Gly Phe Ala Ala Gln Thr Gly Asp Gln His Thr Thr Ala Leu Gln Tyr	1171	
gcg cgc aag aag aaa ctg cag aag aag ggc tgc gac ctg atg tgt aat	Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn	1219	
gag ttg ggc atg ggc aaa gtc ttg ggc caa aag cac aat gag ggc tcg	Gln Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Gln Gly Trp	1267	
att ttg gat gct cac ggt ggt gta gtc gat gtc gag cac ggc agc aaa	Ile Leu Asp Ala His Gly Gly Val Val Asp Val Gln His Gly Ser Lys	1315	
atc gag gtt gct gcg caa att ttg gac gcg gca ctg gcg tat cgc gaa	Ile Gln Val Ala Ala Gln Ile Trp Asp Ala Leu Ala Tyr Arg Gln	1363	
gtc tagaaaaatc cagctagacc act	Val	1389	
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	10		
	15		
Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val	20		
	25		
Arg Ala Phe Lys Gln Ala Gly Asp Asn Val Arg Val Val Pro Thr Gln	35		
	40		
	45		



Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys  
 370 375 380  
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val  
 385 390 395 400  
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala  
 405 410 415  
 Leu Ala Tyr Arg Glu Val  
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 <212> DNA  
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 <223> RXA00581

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 115 Met Ala Glu Gln Asn  
 1  
 gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca gat ttc  
 163 Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe  
 20  
 agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac  
 211 Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn  
 35  
 tca atg cct cag gtg acc caa aaa gaa gtc att gaa ctt cga ggc  
 259 Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly  
 40  
 atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg  
 307 Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro  
 55  
 ctg tcc cgt ctg att cac ctc cag gta ggc gca cga cag caa ctt act  
 355 Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr  
 70  
 gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtc ccg  
 403 Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro  
 90  
 ttt gtc att ggt gtc ggc gga tcc gtc gtc ggc gtc ggt aaa tca acc acc  
 451 Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr  
 105  
 gcc cga ctc ctc caa gtc ctc cag cgc tgg aat tcc cac ccc ccg cgc  
 499 Ala Arg Leu Leu Gln Val Leu Gln Arg Trp Asn Ser His Pro Arg  
 120  
 125  
 130

gcatgagttt actcacgtgc ccaagtcctt tagccaccca ttgaagtga aataataccc 60  
 cgatcacact agtggagtag ctaagtgca caatgatc atg gca gag caa aac  
 115 Met Ala Glu Gln Asn  
 1  
 gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca gat ttc  
 163 Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe  
 20  
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 211 Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn  
 35  
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 259 Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly  
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 307 Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro  
 55  
 ctg tcc cgt ctg att cac ctc cag gta ggc gca cga cag caa ctt act  
 355 Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr  
 70  
 gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtc ccg  
 403 Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro  
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 451 Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr  
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 gcc cga ctc ctc caa gtc ctc cag cgc tgg aat tcc cac ccc ccg cgc  
 499 Ala Arg Leu Leu Gln Val Leu Gln Arg Trp Asn Ser His Pro Arg  
 120  
 125  
 130

547 ggt gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc ggc gaa cta  
 Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu  
 135  
 140  
 145  
 595 atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac  
 Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp  
 165  
 160  
 175  
 643 caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc  
 Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu  
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 195  
 691 gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca  
 Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro  
 200  
 205  
 739 ggc gaa ttc acc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc  
 Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly  
 210  
 225  
 787 tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc  
 Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe  
 230  
 235  
 835 gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg  
 Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp  
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 255  
 883 tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc  
 Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro  
 265  
 270  
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 931 ggt gcc cca ttc tcc cat tac gcc gac atg gct gat cca gac tcc atc  
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile  
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 979 gcc gtc gct cga gaa cgt tgg caa tgc atc aac ctc gac aac ttg gtc  
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val  
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 305  
 1027 gag aat att ctt ccc acc cga gtt cgc gcg tgc ttg gta ctg aaa aaa  
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys  
 310  
 315  
 320  
 1069 ggt agc gat cac ttg gtc gaa cgc gtc agt agc atg cgc aag atc  
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>222> (101) .. (1000)
>223> RXS00838
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Met Lys Ile Ala Ile  
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211 tct ggt gca gat atc acg atg gtc gca cgt gga cga aca tta gaa gcc Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala 25 30 35

307 gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat  
Val Pro Ile Pro Ala Val Ala Ser Val Gln Gln Leu Lys Asp Ala Asp

403	gaa	ctt	ctg	ggt	ggg	ata	cct	gcg	aat	tcg	gtg	gtc	gca	att	act	cag
	Glu	Leu	Leu	Gly	Gly	Ile	Pro	Ala	Asn	Ser	Val	Val	Ala	Ile	Thr	Gln
	90									95					100	

499	cgt gtc tgc	120	Arg Val Trp
	ctg cct ggt		Pro Gly Val
	gtc gtc gtc	125	Val Arg Val
	ggt ggc ggc		Gly Phe Phe
	ttc ttc gtc		Val His Val
	cat gat gag	130	
	cca ggg ggg		Pro Gly Pro

150	Ser Gly Gln Leu Ser Arg Gln Phe Ala Ser Thr Leu Gln Ala Gly	165
155	tct ggt gaa ctt tct agg caa ttc gca agc act cct gaa cag gcc ggt	160
595		

691	gac atg ttc gta gag gtc ttc ggc ggg tgg ggg gct ttc gtc gaa aag	Ala Met Phe Val Gln Val Phe Gly Gly Leu Gly Ala Phe Val Gln Lys	185	190	195	739	caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg	Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Gln Ala Leu	200	205	210	787	atg gaa gag ggt ggt gca gca ggt ggt gtc ggc ttg cgc	Met Gln Gln Val Ala Gln Val Ala Arg Ala Gly Val Ala Leu Pro	215	220	225	835	agc gat gcg gtc gag cgc acc atg aat ttt gcg gat cgg atg cct gag	Ser Asp Ala Val Gln Arg Thr Met Asn Phe Ala Asp Arg Met Pro Gln	230	235	240	245	883	aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtc agt	Asn Ser Thr Ser Met Gln Arg Asp Leu Ala Gly Val Ala Ser	250	255	260	931	gag ctt gag gct cag aca ggt gca atg gtc cgg gca gca gca aag gtc	Gln Leu Gln Ala Gln Thr Gly Ala Ile Val Arg Ala His Lys Val	265	270	275	979	ggt gtc aaa act ccg ctt cat gac ctt att tat gct gct aag ctg	Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu	280	285	290	1023	aaa gaa gag gaa aat tca ctt taggagataga atccaagatcc atg	Lys Gln Gln Gln Asn Ser Leu	295	<210> 630	<211> 300	<212> PRT	<213> Corynebacterium glutamicum	<400> 630	Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Tyr Phe Gly	1	5	10	15	Ala Leu Leu Gln Gln Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly	20	25	30	Arg Thr Leu Gln Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala	35	40	45	Arg Gly Gln Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Gln	50	55	60	Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg	65	70	75	Ser Leu Asp Leu Ala Gln Leu Leu Gly Ile Pro Ala Asn Ser Val	85	90	95	Val Ala Ile Thr Gln Asn Ser Ile Gln Ser Ala Asp Leu Ala Lys	100	105	110	Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
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115 120 125  
 Val His Gln Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser 130 135 140  
 Tyr Thr Phe Gly Asp Ser Gly Gln Leu Ser Arg Gln Phe Ala Ser Thr 145 150 155 160  
 Leu Gln Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val 165 170 175  
 Asp Val Trp Gln Lys Ala Met Phe Val Gln Val Phe Gly Gly Leu Gly 180 185 190  
 Ala Phe Val Gln Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala 195 200 205  
 Ser Leu Gln Ala Leu Met Gln Val Ala Gln Val Ala Arg Ala Ala 210 215 220  
 Gly Val Ala Leu Pro Ser Asp Ala Val Gln Arg Thr Met Asn Phe Ala 225 230 235 240  
 Asp Arg Met Pro Gln Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala 245 250 255  
 Ala Gly Val Ala Ser Gln Leu Ala Gln Thr Gly Ala Ile Val Arg 260 265 270  
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 Val Thr Asn Val Ser 1  
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Gln Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 20  
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Gln Leu Leu Asp Lys Val Thr Ser Lys Tyr 35

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gcc ctc gtc atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc
259 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
307 TAC CAT CAG GCA GAT GAG GGA GTA TTC GAG TTC ATC GGA CCA TCG GTT
Tyr His Gln Ala Asp Gln Gly Val Phe Gln Phe Ile Gly Pro Leu Val
65 55
act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc
355 Thr Pro Gln Pro Gly Gln Lys Pro Leu Ser Ile Ala Leu Arg Gln Ile
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35 40 45
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Gln Gly Val Phe Gln Phe
50 55
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Gln Lys Pro Leu Ser Ile
65 70 75 80
Ala Leu Arg Gln Ile Asn Ala Gly Leu Leu Asp His Gln Gln Gly
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Corynebacterium glutamicum
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Val Ser Lys Leu Lys
1
5

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gac tca aga tgc ctc gac gtc ggc tcc ggc gat cca tcc tcc ggc gat cca tcc tcc ggc  
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 163 10 15 20  
 gac ctg gcc ggc cgc cag gtc ggc cat gtc gat gtc gtc gtc gtc gtc gtc gtc gtc gtc  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 211 25 30 35  
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 Ile Asn Thr Thr Phe Gln Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 259 40 45 50  
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 307 55 60 65  
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 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Lys Leu Leu Ile Val  
 355 70 75 80 85  
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 403 90 95 100  
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 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Gln Gln  
 451 105 110 115  
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 Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln Ser Leu His Gln Ile  
 499 120 125 130  
 cga caa ctc acc aag cag ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc ctc  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 547 135 140 145  
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 35 40 45  
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His Met Asn  
 50 55 60



90	95	100
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa	451	451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Gln Gln		
105	110	115
atc tac ccc ttc cct acc aaa gaa gcc tca gag agt ctc cac gaa ata	499	499
Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln Ser Leu His Gln Ile		
120	125	130
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt atc cgc cgt gga	547	547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly		
135	140	145
atc cac ttc cga tac ctc gag tgg aca aag cct taacaagacc	593	593
Ile His Phe Arg Tyr Leu Leu Gln Trp Thr Lys Pro		
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 20 25 30  
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 35 40 45  
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
 50 55 60  
 Ala Gln Gln Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75  
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
 85 90 95  
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110  
 Asn Arg Gln Gln Ile Tyr Pro Phe Pro Thr Lys Gln Pro Ser Gln  
 115 120 125  
 Ser Leu His Gln Ile Arg Gln Leu Thr Lys Gln Leu Pro His Arg  
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 Pro  
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<223> RXA00166

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Val Glu Leu Ala Arg 1  
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ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc  
Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
163  
20  
211  
agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac  
Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
25  
259  
atg ttg cgg gtg ttg phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln  
Met Leu Arg Val Phe Arg Ser Ala Leu Val Pro Cys Trp Gln  
40  
45  
307  
gcg aca gca gaa cac aca gga ata cgt gac aac gcc ggt gat ctg att  
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile  
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355  
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Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala  
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75  
80  
85  
403  
gaa ttt gat cgg gtt gtt gca cct gag ggt gca gtc ctg ctg ctg gtt  
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp  
90  
95  
451  
aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctg acg att cgc att  
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile  
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499  
atg cat gcc ggc gat gta ctc aag cgg gga ttc acc cca gaa acc gca  
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala  
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125  
130  
547  
gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac  
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Trp Asn Gln His  
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145  
595  
ctc acc cct gaa gaa atc atc cag ctg gct cac acg agc tcc tac tgg  
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp  
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160  
643  
tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag  
Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln  
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175  
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Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
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Met Leu Arg Val Phe Arg Ser Ala Leu Val Pro Cys Trp Gln  
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307  
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Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile  
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Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala  
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80  
85  
403  
gaa ttt gat cgg gtt gtt gca cct gag ggt gca gtc ctg ctg ctg gtt  
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp  
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aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctg acg att cgc att  
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile  
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499  
atg cat gcc ggc gat gta ctc aag cgg gga ttc acc cca gaa acc gca  
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gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac  
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Trp Asn Gln His  
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ctc acc cct gaa gaa atc atc cag ctg gct cac acg agc tcc tac tgg  
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp  
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tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag  
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tgg tat ctc tac gag cat ctg ggt ttc agt ccc gac aat cca gtg gaa  
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 Trp Tyr Leu Tyr Gln His Leu Gly Phe Ser Pro Asp Asn Pro Val Gln  
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 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu  
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 Val Pro Cys Trp Gln Ala Thr Ala Gln His Thr Gly Ile Arg Asp Asn  
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 Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val  
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 Thr Ala Ala Ser Ala Gln Phe Asp Arg Val Ile Ala Pro Gln Gly Ala  
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 Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His  
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 Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe  
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 Thr Pro Gln Thr Ala Ala Pro Trp Ile Ile Asp Arg Gln Ile Arg Thr  
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 Thr Trp Asn Gln His Leu Thr Pro Gln Gln Ile Ile Gln Leu Ala His  
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 Thr Arg Ser Tyr Trp Leu Asn Ala Ser Gln Lys Ile Lys Gln Arg Val  
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 Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Gln His Leu Gly Phe Ser Pro  
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 Asp Asn Pro Val Gln Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser  
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 Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu  
 210  
 215  
 220



691	ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	Gly Ser Ser Pro Gln Ala Ile Ser Gln Tyr Leu Arg Ser Met Gln Leu	185	190	195				
739	ctt atc gac gac gag ggc gtc tcc gca atc atc atc gaa ccg atc gtc caa	Leu Ile Asp Gln Ala Val Ser Ala Ile Ile Ile Gln Pro Ile Val Gln	200	205	210				
787	ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc	Gly Ala Gly Met Arg Phe His Asp Val Ala Leu Ile Gln Gly Val	215	220	225				
835	ggc aca ctg tgc aag cac gat cgt ttc ttg atc gtc gat gaa att	Ala Thr Leu Cys Lys His Asp Arg Phe Leu Ile Val Asp Gln Ile	230	235	240	245			
883	ggc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat	Ala Thr Gly Phe Gly Arg Thr Gln Leu Phe Ala Thr Leu Ser Asn	250	255	260	265			
931	ggc cta caa cca gac atc atg tgt gtc aag gcc ctc acc ggt gga	Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	265	270	275	280			
979	ttc atg tcc ttc ggc gct act tta tgc acg gac aag gtc gct caa tta	Phe Met Ser Phe Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu	280	285	290	295			
1027	atc agc acc cca aat ggc gga ggt ggc ctg atg cac ggc ccc act ttt	Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe	295	300	305	310			
1075	atg gct aat cct ctg ggc tgt ggc ggt tgc cat gct tca tta gaa atc	Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Gln Ile	310	315	320	325			
1123	att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa	Ile Gln Thr Thr Gly Met Trp Gln Lys Val Lys Arg Ile Gln Ala Gln	330	335	340	345			
1171	ctt atc gca ggc ctt tcc cca cct caa cac ctt cca ggc ggt gtc gat	Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp	345	350	355	360			
1219	gtc cgg gtt ctc ggc ggc att ggt gtc atc gaa atg gaa cca aat gtc	Val Arg Val Leu Gly Ala Ile Gly Val Ile Gln Met Gln Asn Val	360	365	370	375			
1267	aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc	Asn Val Gln Gln Ala Thr Gln Ala Thr Gln Ala Leu Asp His Gly Val Trp Ile	375	380	385	390			
1315	cgc ccc ttg gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg	Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr	390	395	400	405	410	415	420
1363	tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa	Ser Gln Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Val Lys	410	415	420	425	430	435	440

999 aaa taaaccatgc cactttatc tgt  
Gly Lys

<210> 640  
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<212> PRT  
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<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met

Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys

Ala Ala Ala Glu Lys Glu Ile Asp Thr Met Ser His Val Met Phe Gly

Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn

Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser

Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Glu Ala Ser Lys Gly

Glu Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr

His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly

Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Glu Ile Phe Ala Pro

Ala Pro Pro Val Arg Gly Ser Ser Pro Glu Ala Ile Ser Glu Tyr Leu

Arg Ser Met Glu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile

Glu Pro Ile Val Glu Ala Gly Gly Met Arg Phe His Asp Val Ala

Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu

Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe

Ala Thr Leu Ser Asn Gly Leu Glu Pro Asp Ile Met Cys Val Gly Lys









259	atc cca gac	40	Ile Pro Asp	45	gaa tta gaa	30	gaa tta gaa	35	gaa tta gaa
	gag gaa gaa	55	gaa gaa gaa	60	gaa gaa gaa	80	gaa gaa gaa	85	gaa gaa gaa
	gag gaa gaa	70	gaa gaa gaa	75	gaa gaa gaa	90	gaa gaa gaa	100	gaa gaa gaa
	gag gaa gaa	105	gaa gaa gaa	110	gaa gaa gaa	115	gaa gaa gaa	120	gaa gaa gaa
	gag gaa gaa	125	gaa gaa gaa	130	gaa gaa gaa	135	gaa gaa gaa	140	gaa gaa gaa
	gag gaa gaa	145	gaa gaa gaa	150	gaa gaa gaa	155	gaa gaa gaa	160	gaa gaa gaa
	gag gaa gaa	165	gaa gaa gaa	170	gaa gaa gaa	175	gaa gaa gaa	180	gaa gaa gaa
	gag gaa gaa	185	gaa gaa gaa	190	gaa gaa gaa	195	gaa gaa gaa	200	gaa gaa gaa
	gag gaa gaa	205	gaa gaa gaa	210	gaa gaa gaa	215	gaa gaa gaa	220	gaa gaa gaa
	gag gaa gaa	225	gaa gaa gaa	230	gaa gaa gaa	235	gaa gaa gaa	240	gaa gaa gaa
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	gag gaa gaa	685	gaa gaa gaa	690	gaa gaa gaa	695	gaa gaa gaa	700	gaa gaa gaa
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	gag gaa gaa	765	gaa gaa gaa	770	gaa gaa gaa	775	gaa gaa gaa	780	gaa gaa gaa
	gag gaa gaa	785	gaa gaa gaa	790	gaa gaa gaa	795	gaa gaa gaa	800	gaa gaa gaa
	gag gaa gaa	805	gaa gaa gaa	810	gaa gaa gaa	815	gaa gaa gaa	820	gaa gaa gaa
	gag gaa gaa	825	gaa gaa gaa	830	gaa gaa gaa	835	gaa gaa gaa	840	gaa gaa gaa
	gag gaa gaa	845	gaa gaa gaa	850	gaa gaa gaa	855	gaa gaa gaa	860	gaa gaa gaa
	gag gaa gaa	865	gaa gaa gaa	870	gaa gaa gaa	875	gaa gaa gaa	880	gaa gaa gaa
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BGI-121CP

979	ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctg	gly gly arg glu leu thr leu gln ala leu	280	285	290
1027	ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctg	leu gly gly ile asn ala met ile val gly asn tyr leu thr thr leu	295	300	305
1075	ggc cgc cca atg gaa gat gac ctg gac atg atg gat cgt ctg cag ctg	gly arg pro met glu asp asp leu asp met met asp arg leu gln leu	310	315	320
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<400> 644
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20  
25  
30

	Leu Pro Glu Gln Ile Pro Asp Leu Met Gln Leu Ala His Gln Val	35
		40
		45

Arg Leu Lys Trp Cys Gly Gln Gln Ile Gln Val Gln Gly Ile Ile Ser  
50 55 60

Amino acid	Protein	Frequency (%)
Leu Lys Thr Gly Gly Cys	Pro Gln Asp Cys His Phe Cys Ser Gln Ser	65 70 75 80

Gly Leu Phe Gln Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn

Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe  
100 105 110

Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln	115	120	125
---	-----	-----	-----

130	135	140
Leu Gln Gln Ala Val	Leu Ala Ile His Ser Gln Val	Gln Ile Gln Val

Ala Ala Ser Ile Gly Thr Leu Asn Lys Gln Gln Val Asp Arg Leu Ala 145  
150  
155  
160

Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser	165	170	175
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Tyr Phe Pro Gln Val Val Thr Thr His Thr Thr Trp Gln Gln Arg Arg Gln

Thr Leu Arg Leu Val Ala Gln Ala Gly Met Gln Val Cys Ser Gly Gly 195  
 Ile Leu Gly Met Gly Gln Thr Leu Gln Arg Ala Gln Phe Ala Val 210  
 Gln Leu Ala Gln Leu Asp Pro His Gln Val Pro Met Asn Phe Leu Asp 225  
 Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Gln Leu Met Asp Ser Arg 245  
 Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr 260  
 Met Leu Arg Phe Ala Gly Gly Arg Gln Leu Thr Leu Gly Asp Lys Gly 275  
 Ser Gln Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn 290  
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Gln Asp Asp Leu Asp Met Met 305  
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 Met Arg Gln Val Ala 1  
 gca gct gcg tgg atg gaa aac gcg cag gca tgg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Gln Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln 20  
 Tac ggt tcg ggg cgt aag gcg agc agc gtc gcg gat tcg gct cgt gaa 211  
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Gln 35  
 gaa att gct tct ctg ctg ggc tgt gaa cct atc gag gtc gtg ttc acc 259  
 Gln Ile Ala Ser Leu Leu Gly Cys Gln Pro Ile Gln Val Val Phe Thr 50  
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tca ttc cac 307  
 Ala Ser Gly Thr Gln Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His 65

[illegible]

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 310 315 320 325  
 1123 cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc  
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Glu Glu Ser  
 330 335 340  
 1171 atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt  
 Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg  
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 1212 act gcg gga atg gct ttt tagcgaccgt aatcgcata gtg  
 Thr Ala Gly Met Ala Phe  
 360

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 Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
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 35 40 45  
 Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60  
 Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80  
 Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95  
 Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110  
 Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
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 Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
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 Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160  
 Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175  
 Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190  
 Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205



307	cgc att atc gga gga gga cgc ccc aca cag gtg acg ttt acg tct ggt gga	Arg Ile Ile GLY GLY GLY Arg Pro Thr Gln Val Thr Phe Thr Ser GLY GLY	55
355	tca gaa gcc aac aac ctc gct atc aaa gga ggc tgc tta gct aat cct	Ser Gln Ala Asn Asn Ala Asn Pro	85
403	cgt ggc cgc cgc ctc atc acc acc cgc atc gag cat gac agt gtc cta	Arg GLY Arg His Leu Ile Thr Thr Val Leu	100
451	gaa act gct gct gct tat ctt gaa agt ttt cat gat ttc gag atc tac	Gln Thr Ala Ala Tyr Leu Gln Arg Phe Gln Ile Thr Tyr	115
499	cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	Leu Ser Pro Asp His Thr GLY Leu Ser Pro Gln GLY Leu Arg Lys	120
547	gca gtc agc agc gac acc aca tgc atc agc att ggt tat gcc aac aat	Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile GLY Tyr Ala Asn Asn	145
595	gag gtg gga acc att cag ccg ata gct gag tgc ccg gag gta agc agt	Gln Val GLY Thr Ile Gln Pro Ile Ala Gln Leu Ala Val Ser Ser	165
643	acg cct ttt cac acc gat gca gta gct gca cat tta acc ttt gac	Thr Pro Phe His Thr Asp Ala His Leu Thr Phe Asp	180
691	ttg gga gct gac ggc tca agt ttg tgc ggt ggt cat aaa ttc ggt gcc cct	Leu GLY Val Asp Ala Leu Ser Leu Ser GLY His Lys Phe GLY Ala Pro	195
739	aaa ggg att gga gtg tca tgg tca aag ctt ccc ctg gag ccg gta atc	Lys GLY Ile GLY Val Leu Trp Ser Lys Leu Pro Leu Gln Pro Val Ile	210
787	cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt ggc acg gaa aac gtt	His GLY GLY GLY Gln Gln Lys Arg Ser GLY Thr Gln Asn Val	225
835	gcg ggg gct atc gcc ttt gcc act ggc tgg gaa tgc ggc agg ggc gaa	Ala GLY Ala Ile Ala Phe Ala Thr Ala Leu Gln Leu Ala Arg Ala Gln	245
883	tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	Ser Tyr Pro Asp Leu GLY Gln Phe Ile Gln Val Leu Thr Ile Pro	260
931	gga gca cac ctc act gga cat cct agg atg cgc att gat gga cac gca	Gly Ala His Leu Thr GLY His Pro Arg Met Arg Ile Asp GLY His Ala	275
979	tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	Ser Phe Leu Phe Asp Ser Ile GLY Ser Gln Thr Val Leu Gln Leu	290
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 163 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr 20

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 211 Leu Asn Ser His Gln Ile Pro Gln Val Pro Gln Arg Val Ala Ser Gly 35

glt gcg gcg ggt ttc cgc acc cat gcg cag att tct gag gtg acg tgg  
 259 Val Ala Ala Phe Arg Thr His Ala Gln Ile Ser Gln Val Thr Ser 50

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 307 Gln Pro Ile Ala Val Asp Gln Leu Gln Ala Ala Arg Gln Ala Val Ala 65

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 355 Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg 85

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 403 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Phe Val Arg 100

cga aaa gcg ggc ggt gttg ttg ttg cgc ggc gag gac ggc gag tgg acc  
 451 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Trp Leu Thr 115

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 499 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Gln Pro Asp 130

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 547 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln Lys Leu Val Asp 145

gag tgg acg cgc cttg gttg ctc agc ggc ggc cac cgg cttg ctc ggc  
 595 Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly 165

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 643 Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser 180

cgt gcc tgg gttg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691

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Arg Ala Trp	Val	Leu	Val	Asp	Ala	Thr	Thr	Tyr	Ala	Ala	Tyr	Arg	Pro	185		
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GenBank accession number: F01011.1  
 Date of release: 1998-07-01  
 Version: 1.0

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100	Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp	100
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145	Gln Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala	145
165	His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys	165
180	Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr	180
195	Ala Ala Tyr Arg Pro Leu Arg Leu Asp Gln Trp Gln Ala Asp Ile Val	195
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 145 150 155  
 Gln Asp Gly Arg Ile Asp Leu Asp Ser Leu Gln Leu Asp Gln Thr Val  
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 Lys Val Val Ala Phe Thr His Gln Ser Asn Val Thr Gly Ala Val Ala  
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 Asp Val Pro Gln Leu Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr  
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 Gly Pro Leu Thr Ala Gln Arg Gly Gly Ala Ile Ser Phe Gly Val  
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 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser  
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120 125 130

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355	cgt gag gca acc ttc atc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	70	Arg Gln Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Cys	85
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547	tgg ctc tac tca gaa gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	135	Trp Leu Tyr Ser Gln Val Val Arg Lys Ile His Gln Leu Asn Pro His	145
595	acc ggt gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	150	Thr Gly Val Gln Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu	165
643	ctg cag gaa gtc ttc gaa tcc cgc cca gag gtc ttc gct cac aac gtc	170	Leu Gln Gln Val Phe Gln Ser Arg Pro Gln Val Phe Ala His Asn Val	180
691	gaa act gtc cca cgt atc ttc aag cgc atc cgc cca gca ttc cgc tac	185	Gln Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr	195
739	gag cgt tca ctt gat gtc atc cgt cgt cag gct cgc gat ttc gtc gtc	200	Gln Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val	210
787	acc aag tcc aac ctg atc ttc ggc atg ggt gaa acc aag gaa gaa atc	220	Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Gln Thr Lys Gln Gln Ile	225
835	acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc	230	Thr Gln Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr	245
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979	atg ggc ttc gct gct gtc atg tcc ggc cca ttc gtc cgt tcc tct tac			



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 Pro Leu Asp Arg Gly Gln Pro Leu Arg Val Ala Gln Ser Val Arg Gln  
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 Gly Lys Lys Asp Leu Leu Gln Val Phe Gln Ser Arg Pro Gln Val  
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 Met Thr Ala Pro Arg 1  
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 Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Gln Pro 20  
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 Ile Gln Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Gln Ala Trp Asp 35  
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 45  
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 tat caa gca gag ctt gct acc cgt agt gct aat gat gaa atc cct gat 259  
 Tyr Gln Ala Gln Leu Ala Thr Arg Arg Ala Asn Asp Gln Ile Pro Asp

acc	cag	cgg	gaa	gat	ctt	ccc	acc	aac	gga	ctg	ccg	gtg	atc	aat	gct	355
Thr	Gln	Pro	Gln	Asp	Leu	Pro	Thr	Asn	Gly	Leu	Pro	Val	Ile	Asn	Ala	
70					75					80					85	

	451	tat ccg atc atc aaa tta gcc gat cgc atc gat gtc gat tca gta	Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val	105	110	115
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947 Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala

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65 70 75 80

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Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
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Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
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Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
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Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln 20  
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Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu 35  
211

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Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Asp  
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Gene: *gag*  
Accession: F01001.1  
Version: 1  
Date: 1990-01-01  
Source: HIV-1  
Organism: *HIV-1*  
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Val Thr Phe Asn Tyr 1  
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Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly 20  
ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa atc cat gtt 211  
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Ile His Gly 25  
cct gga aac ttc aag gat gct aag act ctt gag gtt ctc acc gac gtt aag 259  
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys 40  
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Ser Phe Glu Glu Glu Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val 100  
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Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu 120  
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Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys 145  
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Lys Met Gly Val Lys Leu Pro Gly His Ala Thr Thr Ala Val Arg 165  
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac 643  
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Glu Lys Lys Gly Ser Asp 180  
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Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe 195

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 787 Thr Gln Arg Gly Ala Ile Gln Ile Asp Asp Tyr Met Arg Thr Asn Val  
 gat ggc att tac gcc atc ggt gac gtt acc gcc aag ctt cag ctt gct  
 835 Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Ala  
 cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt  
 883 His Val Ala Gln Ala Gln Gly Ile Val Ala Ala Gln Thr Ile Ala Gly  
 gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc  
 931 Ala Gln Thr Gln Thr Leu Gly Asp Tyr Met Met Met Met Pro Arg Ala Thr  
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gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac 163  
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Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Ser Thr 35  
cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa cgc ttg 259  
Arg Gln Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu 50  
acc act cty gty cac ctg acc ctg gtt aac cac act cgc gaa gag atg 307  
Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Gln Gln Met 65  
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg 355  
Lys Ala Ile Leu Arg Gln Tyr Leu Gln Leu Gly Leu Thr Asn Leu Leu 85  
gcg ctt cga gga gat cgc cct gga gag cca tta ggc gat tgg gtg agc 403  
Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 100  
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739	acg agc ctg cgg tct gtc cgt cga cag gtc gaa ctc tct ggt gtc caa	200	205	210
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883	acc aat atg gca gag cga ctc att gcc gaa ggt ggc gaa gat ctg cac	250	255	260
931	ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtc tgc tac aac	265	270	275
979	ctt ggc atg ggc cct gct tgg gga gca gag cac ggc caa gac ggc gtc	280	285	290
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	Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His	50	55	60
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Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro 180  
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Gly Ile Gln Tyr Ser Thr Asn Met Ala Gln Arg Leu Ile Ala Gln Gly 245  
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Ala Gln Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln 260  
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Gln Gln Leu Arg Thr Lys Leu Arg Gln Ala Arg Thr Asn Met Asp Gln 20  
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 Ile Gln Gln Pro Gln Gly Thr Arg Leu Gly Pro Gln Ala Leu Asn Phe 115  
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 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile 130  
 agc cta ggt aaa ggt ggc ggt ttc tac gac gcc gct cta gcc acc gga 547  
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly 145  
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 Ala Tyr Val Pro Val Arg Thr Gln Pro Gly Gly Arg Leu Leu Asp 50  
 Ala Leu His Ala Gln Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Gln



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 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Gln Gly Pro Thr Ser Leu Val  
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 Pro Gly Ala Phe Gly Ile Gln Gln Pro Gly Gly Thr Arg Leu Gly Pro  
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 Gln Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
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 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg  
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 Trp Ala Leu Tyr Gln Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
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 95  
 100

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 Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly  
 135 140  
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&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 678

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Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala  
 35 40 45

Ala Tyr Val Pro Val Arg Thr Gln Pro Gly Gly Arg Leu Leu Asp  
 50 55 60

Ala Leu His Ala Gln Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Gln  
 65 70 75 80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Gln Gly Pro Thr Ser Leu Val  
 85 90 95

Pro Gly Ala Phe Gly Ile Gln Gln Pro Gly Gly Thr Arg Leu Gly Pro  
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Gln Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
 115 120 125

Thr Pro Ser Gly Ile Arg Leu Lys Gly Gly Gly Phe Tyr Asp Arg  
 130 135 140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn  
 145 150 155 160

Gly Gln Ile Arg Asp  
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&lt;211&gt; 579

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 Met Ile Gly Ala Ile  
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 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro  
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tgg cac atc ccc gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Thr Thr Met Gly  
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 Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr  
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ccc gtc ttc tac gca ccc gaa atc ccg ggc aac ttc aac ctc gat gac gaa 499  
 Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe Asn Leu Asp Asp Gln  
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tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
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 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser 50  
 Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Thr Val Thr Gln 65  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gln Val Tyr Lys Ala 85  
 Thr Val Gly Ser Ala Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr 100  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe 115  
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 Lys Phe Gln Arg Tyr Ile Lys Val 145  
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 Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val 35  
 gcg aag tgg tgg ttc cta gct gag cgt gag ggt tgg att act gag 259  
 Ala Lys Leu Ser Ser Phe Leu Ala Gln Arg Gly Gly Trp Ile Thr Gln 50  
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Ile	Leu	Pro															739	
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Ile	His	His																787
215																		
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Asp	Ala	Glu	Lys	Gln	Val	Leu	Ala	Arg	Gly	Leu	Arg	Phe	His	Leu	Glu			979
280																		
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Asp	Arg	Val	Leu	Val	Tyr	Gly	Asn	Arg	Thr	Val	Val	Phe	Asp					1021



305	Val Phe Asp	
290	Arg Phe His Leu Gln Asp Arg	295
285	Gln Arg Leu	275
280	Ala Asp Arg	280
275	Gly Arg	285
270	Val Leu Val	290
265	Val Tyr	300
260	Val Leu Val	
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10	Val Leu Val	
5	Val Leu Val	
0	Val Leu Val	

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 Val Leu Ala Arg Gly Leu Arg phe His Leu Gln Asp Arg Val Leu Val  
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cgc 582

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20 His Gln Asn Leu Arg Tyr Ile Ala Gln Asn His Asn Val Pro phe phe  
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35 His Val Pro phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala phe Asp  
 40 45

50 Gln Val Ala Gln Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
 55 60

65 Ala Arg phe Met Gln Ile Leu Pro Pro Asp Leu Cys Gln Met Trp Ala  
 70 75 80

85 Gly Arg Val Leu Asn Ile His His Ser phe Leu Pro Ser phe Met Gly  
 90 95

100 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
 105 110

115 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
 120 125

130 Gln Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Gln Met  
 135 140

145 Gln Arg Leu Gly Arg Asp Ala Gln Lys Gln Val Leu Ala Arg Gly Leu  
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165 Arg phe His Leu Gln Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
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Val phe Asp

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 Val Thr Ala Ile Lys 1

163 ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag  
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211 cgc gtt gct gcg ttg aag gag aaa ggg att gtc ccg ggg ctt gcc acc  
 Arg Val Ala Ala Leu Lys Gln Lys Gly Ile Val Pro Gly Leu Ala Thr 35

259 gtg ctg gtc gtc ggt gat gac cca ggc agc cac tct tac ttg aag atg aag  
 Val Leu Val Gly Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys 50

307 cat cgt gac tgt gag cag att ggt gtc aac tgc atc cgt aag gat ctg  
 His Arg Asp Cys Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu 65

355 cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg  
 Pro Ala Asp Val Thr Gln Gln Leu Phe Ala Val Ile Asp Gln Leu 85

403 aac aac gat gat tct tgc act ggt tac att gtc cag ctt cct ttg cct  
 Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro 100

451 aag cac ttg gac gaa aac gct gtc gtc gag cgc att gat cca gct aag  
 Lys His Leu Asp Gln Asn Ala Val Leu Gln Arg Ile Asp Pro Ala Lys 115

499 gat gct gat gtc gtc ctc gta aac ctg ggc aag ctt gtc ctc aac  
 Asp Ala Asp Gly Leu His Pro Val Asn Leu Lys Leu Val Leu Asn 130

547 gag cca gct cca ctg cca tgc acc cgc aat ggt tcc atc agc ttg ttg  
 Gln Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu 145

595 cgt cgt ttc ggc gtc gag ctt gat ggc ggc aag gtc gtc atc ggc  
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643 cgt ggc gtc acc gtc ggt gtc ggc cca att ggc ctg atg ctg acc cgc cgt  
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691 tcc gag aac tcc acg gtc act ttg tgc cac act ggc acg aag gat ctg  
 Ser Gln Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu 195

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	Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser	35	40	45	
	Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser	50	55	60	
	Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala	65	70	75	80
	Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val	85	90	95	
	Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg	100	105	110	
	Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly	115	120	125	
	Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly	130	135	140	
	Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys	145	150	155	160
	Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu	165	170	175	

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Gly Thr Lys Asp Leu Ala Ala Gln Thr Arg Ala Ala Asp Val Ile Ile  
195 200 205  
Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro  
210 215 220  
Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu  
225 230 235 240  
Leu Gly Asp Val His Pro Asp Val Trp Gln Val Ala Gly Ala Val Ser  
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Val Asp Asn His Ala  
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Ala Val Arg Gln Phe Asp Gln Arg Ala Thr Ala Ile Arg Gln  
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Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Gln Thr Phe Ala Gly Leu  
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His Gln Asp Pro Thr Thr Val Leu Gln Lys Thr Phe Ser Gln Gly His  
55 60 65  
gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355  
Gln Gln Leu Val Leu Val Arg Gln Ile Pro Ile Tyr Ser Met Cys Gln  
70 75 80 85  
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His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro 90 95 100  
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 Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala 105 110 115  
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 Asp Met Phe Ala Lys Arg Pro Gln Val Gln Gln Arg Leu Thr Ser Gln 120 125 130  
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 Ile Ala Asp Ala Leu Val Gln Lys Leu Asp Ala Gln Ala Val Ala Val 135 140 145  
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 Val Ile Gln Ala Gln His Leu Cys Met Ala Met Arg Gly Ile Arg Lys 150 155 160 165  
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 Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Phe Lys Asn 170 175 180  
 aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688  
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 Gln Gly Leu Leu Gln Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Gln 35 40 45  
 Thr Phe Ala Gly Leu His Gln Asp Pro Thr Thr Val Leu Gln Lys Thr 50 55 60  
 Phe Ser Gln Gly His Gln Leu Val Leu Val Arg Gln Ile Pro Ile 65 70 75 80  
 Tyr Ser Met Cys Gln His His Leu Val Pro Phe Phe Gly Val Ala His 85 90 95  
 Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys 100 105 110  
 Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Gln 115 120 125  
 Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Gln Lys Leu Asp Ala 125

130 145 160 175 180 185 190 195  
 Gln Ala Val Ala Val Ile Gln Ala Gln His Leu Cys Met Ala Met  
 Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Ser Ala Val Arg  
 Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Gln Val Phe Ser Leu  
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 <213> Corynebacterium glutamicum  
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 <223> RXA01516  
 <400> 689  
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 gttgatgttg ccgcatgtg gcgaagtga ggaactcacc atg gct gat cgt att  
 115 Met Ala Asp Arg Ile  
 1 Met  
 gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt  
 163 Gln Leu Lys Gly Leu Gln Cys Phe Gly His His Gly Val Phe Asp Phe  
 20  
 gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg  
 211 Gln Lys Gln Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met  
 35  
 gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat  
 259 Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp  
 40 45 50  
 tac ggc ggc ttg gca ttg ttg ggt gct gaa atc gtg gaa ggc cca tcc  
 307 Tyr Gly Ala Leu Ala Leu Leu Val Ala Gln Ile Val Gln Gly Pro Ser  
 55 60 65  
 agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg  
 355 Arg Asp Leu Ile Gln Thr Val Ala Thr Gln Ser Ala Asp Ala Val Met  
 70 75 80 85  
 gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc  
 403 Ala Lys Phe Asp Ala Leu His Ala Val Gln Val Thr Ile His Lys Pro  
 90 95 100  
 aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gct gcc cga  
 451 Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg  
 105 110 115  
 cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgatgc  
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Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala  
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130  
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513

<210> 690

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

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20  
25  
30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu  
35  
40  
45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Val Ala Glu Ile  
50  
55  
60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser  
65  
70  
75  
80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val  
85  
90  
95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
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Asn Ala  
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<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(952)

<223> RXA01515

<400> 691

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Met Asn Val Ser Ser  
1  
5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
10  
15  
20

211	gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg	25	gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg	35	gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg	211
259	atc gcg cat gcc aag gaa tgg gtt ggt ggt ggc ggc gac att gat	40	atc gcg cat gcc aag gaa tgg gtt ggt ggt ggc ggc gac att gat	50	atc gcg cat gcc aag gaa tgg gtt ggt ggt ggc ggc gac att gat	259
307	gag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	55	gag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	65	gag ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	307
355	gtg gaa cgg gac cgg gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	70	gtg gaa cgg gac cgg gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	80	gtg gaa cgg gac cgg gtc gtc gtc gtc gtc gtc gtc gtc gtc gtc	355
403	ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtc ggc gac gtc	90	ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtc ggc gac gtc	95	ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtc ggc gac gtc	403
451	ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	105	ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	110	ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	451
499	gct gat cct gag atg ttt tct gtc atg ggc gaa ggc gaa gtc gtc gtc	120	gct gat cct gag atg ttt tct gtc atg ggc gaa ggc gaa gtc gtc gtc	125	gct gat cct gag atg ttt tct gtc atg ggc gaa ggc gaa gtc gtc gtc	499
547	tgt tgg atg cac tgg cgc acc ctc caa ttc ggt gat ggc gaa gtc gtc	135	tgt tgg atg cac tgg cgc acc ctc caa ttc ggt gat ggc gaa gtc gtc	140	tgt tgg atg cac tgg cgc acc ctc caa ttc ggt gat ggc gaa gtc gtc	547
595	gca gat cac ggt gga gac ggt gta ggc gat gtc gtc gtc gtc gtc gtc	155	gca gat cac ggt gga gac ggt gta ggc gat gtc gtc gtc gtc gtc gtc	160	gca gat cac ggt gga gac ggt gta ggc gat gtc gtc gtc gtc gtc gtc	595
643	gat ctt gtc gcc ggc acc gct gct gct gct gct gct gct gct gct gct	170	gat ctt gtc gcc ggc acc gct gct gct gct gct gct gct gct gct gct	175	gat ctt gtc gcc ggc acc gct gct gct gct gct gct gct gct gct gct	643
691	gtg ctt gat cca ggt tgg ggt ttt gcc aaa tca cgt gaa gac aac tgg	185	gtg ctt gat cca ggt tgg ggt ttt gcc aaa tca cgt gaa gac aac tgg	190	gtg ctt gat cca ggt tgg ggt ttt gcc aaa tca cgt gaa gac aac tgg	691
739	cgt tgg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc	200	cgt tgg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc	205	cgt tgg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc	739
787	ctg gtc gga gca tcc cgg aag cga ttc ctg gct ggc gtc gtc gtc gtc	215	ctg gtc gga gca tcc cgg aag cga ttc ctg gct ggc gtc gtc gtc gtc	220	ctg gtc gga gca tcc cgg aag cga ttc ctg gct ggc gtc gtc gtc gtc	787
835	cgt ggc cta gat gtc acc ccc att gat ggc gac cca gca acc gca ggc	235	cgt ggc cta gat gtc acc ccc att gat ggc gac cca gca acc gca ggc	240	cgt ggc cta gat gtc acc ccc att gat ggc gac cca gca acc gca ggc	835
883	gtg acc gca gtc tct gca cat atg gga gca tgg ggt gtc gtc gtc gtc	250	gtg acc gca gtc tct gca cat atg gga gca tgg ggt gtc gtc gtc gtc	255	gtg acc gca gtc tct gca cat atg gga gca tgg ggt gtc gtc gtc gtc	883
931	gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca tgg cga	260	gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca tgg cga	265	gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca tgg cga	931

Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Leu Trp Arg  
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 agt gga gga act cac cat ggc tgatcgatat gaactaaag gcc  
 Ser Gly Gly Thr His His Gly  
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<210> 692  
 <211> 284  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 692  
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 Asp Val Asp Gln Ala Ile Ala His Ala Lys Gln Leu Val Ala Ala Gly  
 35 40 45  
 Ala Asp Met Ile Asp Val Gly Gly Gln Ser Thr Arg Pro Gly Ala Val  
 50 55 60  
 Arg Val Asp Ala Ser Val Gln Arg Asp Arg Val Val Pro Val Ile Lys  
 65 70 75 80  
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
 85 90 95  
 Ser Val Ala Gln Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
 100 105 110  
 Val Ser Gly Gly Leu Ala Asp Pro Gln Met Phe Ser Val Met Ala Gln  
 115 120 125  
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
 130 135 140  
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
 145 150 155 160  
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
 165 170 175  
 Ala Gln Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
 180 185 190  
 Arg Gln Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Gln Phe Ile Ser  
 195 200 205  
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
 210 215 220  
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
 225 230 235 240  
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
 245 250 255



Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val 260  
 270  
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly 275  
 280

<210> 693  
 <211> 859  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(859)  
 <223> RXA02024

<400> 693  
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agcgcgtctc cacaattaag cagtggtctac attagtgtgt atg agt tct ttg ccg 115  
 Met Ser Ser Leu Pro 1

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163  
 Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc 211  
 Gly Ala Thr Phe Gln Asp Thr Ala Ala Leu Asn Arg Ala Ala Gln Val 35

att gaa caa gcc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc 259  
 Ile Gln Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly 50

ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac gcg gtg gtc cca 307  
 Pro Gly Asp Phe Val Ser Ala Gln Gln Ile Asp Arg Val Val Pro 65

atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat atc tct gtc 355  
 Ile Ile Ala Ala Val Arg Gln Arg Phe Pro Asp Ile Asp Ile Ser Val 85

gat acc tgg gcg gcg tcg gtc gat gtc gca gtc gca gtc gca gtc gga 403  
 Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala 100

acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag 451  
 Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Gln Leu Val Gln 115

gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg 499  
 Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly 130

gtg atc cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtc 547  
 Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Ile Val 145

gac gat gta att acg gag acc acc aaa ttg gca gag caa gct gct cgt  
 Ala Asp Val Ile Thr Gln Thr Thr Lys Leu Ala Gln Ala Val Arg  
 150 155 160 165  
 gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc  
 Ala Gly Val Pro Gln Arg Val Phe Ile Asp Pro Thr His Asp Phe  
 643 170 175 180  
 ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag  
 Gly Lys Asn Thr Phe His Gly Leu Gln Leu Arg Arg Ile Asp Gln  
 691 185 190 195  
 gtg gtt gcc acc ggc ttg cgg gtg ctg atg gcc ttg agt aat aag gat  
 Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp  
 739 200 205 210  
 ttc att ggg gaa act ttg gaa aag ggc gtc gat aag cgt gct ggc  
 Phe Ile Gly Gln Thr Leu Gln Arg Gly Val Asp Lys Arg Val Ala Gly  
 787 215 220 225  
 acg ctt gct gcc act gcc ttg ggc ggc ggc ggc ggc ggc gct ttt  
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Arg Gly Val Ala Ala Phe  
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 Arg Val His Gln Val Ala Gln Thr  
 859 250

<210> 694  
 <211> 253  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 694

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 Arg Ala Ala Gln Val Ile Gln Gln Gly Ala Gly Ile Val Asp Ile Gly  
 35 40 45  
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Gln Gln Ile  
 50 55 60  
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Gln Arg Phe Pro Asp  
 65 70 75 80  
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
 85 90 95  
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
 100 105 110  
 His Gln Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
 115 120 125  
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
 130 135 140

Phe Asp Ile Val Ala Asp Val Ile Thr Gln Thr Thr Lys Leu Ala 145  
 150 155  
 Gln Gln Ala Val Arg Ala Gly Val Pro Gln Gln Arg Val Phe Ile Asp 165  
 170 175  
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Gln Leu 180  
 185 190  
 Arg Arg Ile Asp Gln Val Val Ala Thr Gly Trp Pro Val Leu Met Ala 195  
 200 205  
 Leu Ser Asn Lys Asp Phe Ile Gly Gln Thr Leu Gln Arg Gly Val Asp 210  
 215  
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Arg 225  
 230 235 240  
 Gly Val Ala Ala Phe Arg Val His Gln Val Ala Gln Thr 245  
 250  
 gctacgatcc acaaccattg atccgcggca aggtcgccgt atg atc ggt ggc att 115  
 Met Ile Gly Ala Ile 5  
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 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro 163  
 20 25  
 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 10 15  
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 25 30 35  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly 211  
 259  
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 40 45 50  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln Ser Leu Pro Phe Lys 259  
 307  
 ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
 60 65  
 Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser Ser Arg Gln Pro Gly 307  
 70 75 80  
 gac tgg tcc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc 355  
 Asp Trp Ser Ala Gly Thr Val Val Thr Gln Ile Pro Lys Ser Gly 355  
 85  
 tgg atc atg ggc ggc gag gtc tac aag ggc acc gtc ggc agc gcc 403

Trp Ile Met Gly Gly Gln Val Tyr Lys Ala Thr Val Gly Ser Ala  
 90 95 100  
 451 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act  
 Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr phe Asp Val Ser Thr  
 105 110 115  
 499 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa  
 Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn phe Asn Leu Asp Asp Gln  
 120 125 130  
 547 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac  
 Ser Gln Trp phe Thr Ser Gly Gln Tyr Arg Tyr Lys phe Gln Arg Tyr  
 135 140 145  
 atc aag gtt taaggagcaa acaacatgag caa  
 Ile Lys Val  
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&lt;210&gt; 696

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 696

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp  
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Gly Thr Asp Met Pro Trp His Ile Pro Gln Asp Leu Lys His phe Lys  
 20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln  
 35 40 45

Ser Leu Pro phe Lys Pro Leu Pro Gly Arg Gln Asn phe Ile Leu Ser  
 50 55 60

Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln  
 65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gln Val Tyr Lys Ala  
 85 90 95

Thr Val Gly Ser Ala Asp Val Leu Gln Ile Thr Leu Ile Asp Ala Thr  
 100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn phe  
 115 120 125

Asn Leu Asp Asp Gln Ser Gln Trp phe Thr Ser Gly Gln Tyr Arg Tyr  
 130 135 140

Lys phe Gln Arg Tyr Ile Lys Val  
 145 150

&lt;210&gt; 697

&lt;211&gt; 1556

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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 <221> CDS  
 <222> (1) .. (1533)  
 <223> RXXA00989  
 <400> 697

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 96 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct  
 20  
 20 asp asp ile thr val asp val thr leu gly glu thr gly leu ser  
 30  
 144 ttg ccc atc gat ctc ggc ggt gta gaa gca cct gcc tcc gag gag  
 40  
 45 leu pro ile asp leu ala gly glu val glu ala pro ala ser glu glu  
 192 atc acc caa gaa gat ttg ctg ggc ctt gcc cag gtg gaa gca gag ttg  
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 192 ile thr glu glu asp leu leu arg leu ala glu val glu ala glu leu  
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 240 gat caa cgt ttg ttg gaa acc aaa att gat ccc act ttc cga cgc atg  
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 75 asp pro thr phe arg arg met  
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 288 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca  
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 95 ser tyr met met asp leu met gly glu pro ala  
 105  
 336 att cac gtg gct ggc acc aac ggt aag acc tcc acc acc cgc atg atc  
 110  
 336 ile his val ala gly thr asn gly lys thr ser thr arg met ile  
 120  
 384 gag tcg ttg ctg cgc gca ttc cac cgc cgc acc ggc arg ttg thr thr ser  
 125  
 432 ccg cac ctg cag ctg gta acc gaa cgc atc ggc att gat ggc aag ccc  
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 480 atc cac cgc cgt gat ttc gtg cgc atc tac gaa gag att aag ccc tac  
 150  
 145 ile his pro arg asp phe val arg ile tyr glu glu ile lys pro tyr  
 160  
 528 atg gag atg acc gac ggc ttg tca gag gcc gag ggc gag gga cgc aag atg  
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 175 met glu met thr asp ala trp ser glu ala glu gly gly pro lys met  
 180  
 576 agc aag ttg gag gca ctc gtg gcc ctc gct gac tac gca gga ggt ttg gcc gag  
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 190 ser lys phe glu ala leu val ala leu ala tyr ala gly phe ala asp  
 624 gct cct gct gac gtc gcc gtc gtc ggc ggt ggc ggt ggc gga cgc tgg  
 200  
 205 ala pro val asp val ala val glu val gly leu gly gly arg trp  
 672 gat gcc act aac gtg atc aac gca gct gtt tcc gtg atc acc ccg gtg  
 asp ala thr asn val ile asn ala ala val ser val ile thr pro val

gga att ggc cta gtg gct aac aac gac gga atc ttg gat tcc gaa aat  
 48 gly ile gly leu val ala asn asn asp gly ile phe asp ser glu asn  
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 96 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct  
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 20 asp asp ile thr val asp val thr leu gly glu thr gly leu ser  
 30  
 144 ttg ccc atc gat ctc ggc ggt gta gaa gca cct gcc tcc gag gag  
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 45 leu pro ile asp leu ala gly glu val glu ala pro ala ser glu glu  
 192 atc acc caa gaa gat ttg ctg ggc ctt gcc cag gtg gaa gca gag ttg  
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 192 ile thr glu glu asp leu leu arg leu ala glu val glu ala glu leu  
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 50  
 240 gat caa cgt ttg ttg gaa acc aaa att gat ccc act ttc cga cgc atg  
 70  
 75 asp pro thr phe arg arg met  
 80  
 288 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca  
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 95 ser tyr met met asp leu met gly glu pro ala  
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 336 att cac gtg gct ggc acc aac ggt aag acc tcc acc acc cgc atg atc  
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 336 ile his val ala gly thr asn gly lys thr ser thr arg met ile  
 120  
 384 gag tcg ttg ctg cgc gca ttc cac cgc cgc acc ggc arg ttg thr thr ser  
 125  
 432 ccg cac ctg cag ctg gta acc gaa cgc atc ggc att gat ggc aag ccc  
 130  
 480 atc cac cgc cgt gat ttc gtg cgc atc tac gaa gag att aag ccc tac  
 150  
 145 ile his pro arg asp phe val arg ile tyr glu glu ile lys pro tyr  
 160  
 528 atg gag atg acc gac ggc ttg tca gag gcc gag ggc gag gga cgc aag atg  
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 175 met glu met thr asp ala trp ser glu ala glu gly gly pro lys met  
 180  
 576 agc aag ttg gag gca ctc gtg gcc ctc gct gac tac gca gga ggt ttg gcc gag  
 185  
 190 ser lys phe glu ala leu val ala leu ala tyr ala gly phe ala asp  
 624 gct cct gct gac gtc gcc gtc gtc ggc ggt ggc ggt ggc gga cgc tgg  
 200  
 205 ala pro val asp val ala val glu val gly leu gly gly arg trp  
 672 gat gcc act aac gtg atc aac gca gct gtt tcc gtg atc acc ccg gtg  
 asp ala thr asn val ile asn ala ala val ser val ile thr pro val

[illegible]

1440	caa gaa gat ctt gct ggc gca gta gaa ctc gct att gaa cta gca gaa	465	gln gln asp leu ala gly ala val gln leu ala ile gln leu ala gln	470	475	480
1488	gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc	485	asp thr asp val gln ser gly ser gly val ile thr gly ser ile	490	495	
1533	gtg acc gcc ggc gat gcg cgc acc ctg ttt gga aag gaa cct gca	500	val thr ala gly asp ala arg thr leu phe gly lys gln pro ala	505	510	
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 698  
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 50 ile thr gln gln asp leu leu arg leu ala gln val gln ala gln leu  
 65 asp gln arg trp leu gln thr lys ile asp pro thr phe arg arg met  
 70 75 80  
 85 ser tyr met met asp leu met gly gln pro gln asn ser phe pro ala  
 90 95  
 100 ile his val ala gly thr asn gly lys thr ser thr thr arg met ile  
 110  
 115 gln ser leu leu arg ala phe his arg arg thr gly arg thr thr ser  
 120 125  
 130 pro his leu gln leu val thr gln arg ile ala ile asp gly lys pro  
 135 140  
 145 ile his pro arg asp phe val arg ile tyr gln gln ile lys pro tyr  
 150 155 160  
 165 met gln met thr asp ala trp ser gln ala gln gly gly pro lys met  
 170 175  
 180 ser lys phe gln ala leu val ala leu ala tyr ala gly phe ala asp  
 185 190  
 195 ala pro val asp val ala val val gln val gly leu gly arg trp  
 200 205

1556 1533 1488 1440

Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val 210  
 Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala 225  
 Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly 245  
 Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Glu Pro Glu 260  
 Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Val 275  
 Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val 290  
 Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp 305  
 Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Val 325  
 Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro 340  
 Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro 355  
 Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala 370  
 Ala His Asn Pro His Gly Ala Ala Leu Gly Ala Leu Asp Arg 385  
 Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp 405  
 Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu 420  
 Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp 435  
 Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val 450  
 Glu Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu 465  
 Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile 485  
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 <212> DNA



<213> Corynebacterium glutamicum

<220>  
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<223> RXA01517

<400> 699

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Met His Ala Val Leu  
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tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gttg 163  
Ser Ile Gly Ser Asn Met Asp Arg Tyr Ala Leu Leu Asn Thr Val  
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atc gag gaa ttc aaa gat gag atc gttg gcg cag tct gcg atc tac tca 211  
Ile Gln Gln Phe Lys Asp Gln Ile Val Ala Gln Ser Ala Ile Tyr Ser  
25 30 35

acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gttg 259  
Thr Pro Pro Trp Gly Ile Gln Asp Gln Asp Gln Phe Leu Asn Ala Val  
40 45 50

ctc gtt gtt gag gtt gag gaa gaa acc ccc atc gag ttg ctc gcg cgt ggc 307  
Leu Val Val Val Gln Gln Thr Pro Ile Gln Leu Leu Arg Arg Gly  
55 60 65

caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg 355  
Gln Lys Leu Gln Ala Gln Arg Val Arg Val Arg Lys Trp Gly  
70 75 80 85

cca cgc acc ctc gat gttg gat atc gttg cag atc att aaa gat ggg gaa 403  
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Gln  
90 95 100

gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct 451  
Gln Ile Leu Ser Gln Asp Pro Gln Leu Thr Leu Pro His Pro Trp Ala  
105 110 115

tgg cag cgt gcc ttc gttg atc cct ttg ttg gaa gaa gca gaa cct gat 499  
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Gln Ala Gln Pro Asp  
120 125 130

gcc gtc ctg cac gcc acg acc att gca gaa cat gttg gat aat ctt gat 547  
Ala Val Leu His Gly Thr Thr Ile Ala Gln His Val Asp Asn Leu Asp  
135 140 145

ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggcttcac 597  
Pro Thr Asp Ile Gln Gly Val Thr Lys Ile  
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gca

600

<210> 700

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

[illegible]

[illegible]

[illegible]



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175	Gln Gln Asp Gln Gln Ile Ile Ala Gln Leu Arg Ser Asn Pro Lys Asp	450
	Val Gln Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala	435
	Leu Ser Ser Ser Pro Gln Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr	420
	Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile	405
	Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala	390
	Thr Arg Gly Gln Ser Tyr Gln Ile Cys Leu Thr Thr Lys Leu Gln Gly	375
	Ser Lys Asp Gln Tyr Leu Asp Lys Ile Arg Arg Ala Gln Gln Leu Ile	360
	Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp	345
	Gln Asp Gln Trp Phe Gln Thr Ile Lys Lys Leu His Asn Leu Val	330
	Ala Ile Ala Val Gln Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Gln	315
	Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg	295
	Val Gly Tyr Val Gly Tyr Gln Leu Lys Ala Gln Ala Gly Ala Arg Ala	280
	Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp	265
	Thr His Asn Val Gly Gln Gly Asp Phe Thr Trp Leu Lys Gln Asp	250
	Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys	235
	Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Ala Gln	220
	Thr Gln Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Val Phe Gln	205
	Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu	185
		180

Gln Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Gln  
 500  
 Leu Gln Pro Arg Ser Pro Ile Gln Cys Val Arg Ala Phe Pro Gln  
 515  
 Gln Ser Met Thr Gln Ala Pro Lys Leu Arg Thr Met Gln Ile Ile Asp  
 530  
 Gln Leu Gln Ala Ala Pro Arg Gln Ile Tyr Ser Gln Gln Tyr  
 545  
 Phe Ser Leu Asp Gln Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565  
 Val Ile Gln Asn Asn His Val Gln Tyr Gln Val Gln Ala Leu Leu  
 580  
 Ala Leu Ser Asp Pro Gln Ala Gln Trp Gln Gln Ile Arg Val Lys Ser  
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 Arg Pro Leu Leu Asn Leu Phe Gln Val Gln Phe Pro  
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 <213> *Corynebacterium glutamicum*  
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 <223> RXA00958  
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 Met Thr His Val Val  
 1  
 ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 10 15 20  
 gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
 Ala Val Ala Gln Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
 25 30 35  
 gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
 Gln Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gln  
 40 45 50  
 cct ggt tac cct gcc gat gcg gac aac atg atg gcg ctg atc gag cgc 307  
 Pro Gln Tyr Pro Ala Asp Ala Gln Asn Met Met Ala Leu Ile Gln Arg  
 55 60 65  
 aca ctc gcc cag att cct tta cta ctg ggt att tgc ctc gcc tac cag gca 355  
 Thr Leu Gln Ile Pro Leu Leu Gln Ile Cys Leu Gln Tyr Gln Ala

70	80	75	1	80	85
ctc atc gaa tac cac ggc ggc aag gtc gag cct tgt ggc cct gtc cac	Leu Ile Glu Tyr His Gly Lys Val Glu Pro Cys Gly Pro Val His	403			
gag acc acc gac aac atg atc ctt act gat gca ggt gtc cag agc cct	Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Glu Ser Pro	451			
gtr ttt gca ggt ctt gcc act gat gtc gag cct gat cat cca gaa atc	Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro His Pro Glu Ile	499			
cca ggc cgc aag gtc cca atg ggc cgt tat cac tca ctg ggc tgc gtc	Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val	547			
gtr gcc cca gac ggt atg gaa tca cta ggt acc tgt tcc tgc gag atc	Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile	595			
ggt gat gtc atc atg ggc gca cgc acc acc gat gga aag gcc att ggc	Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly	643			
ctg cag ttt cac cct gag tca gtc cta agc cca acg ggt cct gtc att	Leu Glu Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile	691			
ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatctgat	Leu Ser Arg Cys Val Glu Leu Leu Ala Asn	744			
tca					
<210> 704					
<211> 208					
<212> PRT					
<213> Corynebacterium glutamicum					
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Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn	1	5	10	15	
Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg	20	25	30		
Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile	35	40	45		
Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met	50	55	60		
Ala Leu Ile Glu Arg Thr Leu Gly Glu Ile Pro Leu Leu Gly Ile Cys	65	70	75	80	
Leu Gly Tyr Glu Ala Leu Ile Glu Tyr His Gly Lys Val Glu Pro	85	90	95		



Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 115 120 125  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Gln Pro  
 130 135 140  
 Asp His Pro Gln Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
 145 150 155  
 Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Gln Ser Leu Gly Thr  
 160 170 175  
 Cys Ser Ser Gln Ile Gly Asp Val Ile Met Ala Ala Arg Thr Asp  
 180 185 190  
 Gly Lys Ala Ile Gly Leu Gln Phe His Pro Gln Ser Val Leu Ser Pro  
 195 200 205  
 Thr Gly Pro Val Ile Leu Ser Arg Cys Val Gln Gln Leu Ala Asn

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 <223> RXA02790  
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 115 Met Gln Pro Val Tyr  
 5  
 gta aag cgc cgc cca cgg ttt att gcc gtg acg atc gct tca ctc atc  
 163 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
 15 20  
 ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg  
 211 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
 25 30 35  
 acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtc cag ctg gtc  
 259 Thr Pro His Asp Tyr Gln Gly Ser Gly Asn Gly Val Val Gln Leu Val  
 40 45 50  
 gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag tgg gaa  
 307 Gln Ile Pro Gln Gly Ser Ser Ile Ser Gln Leu Gly Pro Gln Leu Gln  
 55 60 65  
 gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc  
 355 Gln Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser  
 70 75 80 85

403	aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	90	95	100
451	gaa caa atg aac gca gca gct gca gta gtc gct ctg ctt gat cca gac	Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	105	110	115
499	aac cag gtt gat ctc ctc gac att cac ggc ggc ggc ggc ggc ggc ggc	Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	120	125	130
547	gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	135	140	145
595	gca gcc gtc gtc acc tgc acc gaa ggc tcc ggc aac tgc acc ggc ggc	Ala Ala Val Thr Cys Thr Gln Gly Ser Ala Asn Cys Ile Thr Ala Glu	150	155	160
643	gat ttg cag cag gtt gtc tcc acc gtc tgc ctt gca gaa ttg ggt gtc	Asp Leu Gln Val Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	170	175	180
691	cca gat tgg gca atc gct gct gta gaa gct cgc ggc gga act gat cca aag	Pro Asp Trp Ala Ile Ala Val Gln Ala Arg Gly Thr Asp Pro Lys	185	190	195
739	cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtc gtc gtc gat cca tcc	Arg Leu Gln Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	200	205	210
787	aac gac gcc cag gga atc ctc acc gat ctc atc acg cga tca gca aac	Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	215	220	225
835	cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	His Phe Gln Gln Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	230	235	240
883	act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	Thr Pro Tyr Gln Leu Val Thr Ala Ser Leu Ile Gln Arg Glu Ala	250	255	260
931	cca gca gga gat ttt gat aag gtc ggc ggc gtc atc ttg aac cgt ctg	Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	265	270	275
979	gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	Ala Gln Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	280	285	290
1027	tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc	Ser Gln Gln Gln Val Ala Thr Thr Asp Gln Asp Arg Gln Thr Val Thr	295	300	305
1075	cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc	Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala	310	315	320
325					

1123 gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga  
 Ala Val Ser Thr Gln Ala Leu Gln Ala Met Gln Asn Pro Ala Gln Gly  
 330 335 340  
 1171 aac tgg ctg tac ttg gtc acc atc gac acc gat gga acc acc gtc ttc  
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Val Phe  
 345 350 355  
 1219 aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac  
 Asn Asp Thr Phe Gln His Gln Ala Asp Ile Gln Gln Ala Leu Asn  
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 Ser Gly Val Leu Asp Ser Asn Arg  
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 <211> 381  
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 <213> Corynebacterium glutamicum

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 Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Gln Gly Ser Gly Asn Gly  
 35 40 45  
 Val Val Gln Leu Val Gln Ile Pro Gln Gly Ser Ser Ile Ser Gln Leu  
 50 55 60  
 Gly Pro Gln Leu Gln Arg Asp Ile Val Ala Thr Asn Ser Ala Phe  
 65 70 75 80  
 Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly  
 85 90 95  
 Phe Tyr Arg Leu Gln Gln Met Asn Ala Ala Ala Val Ser Ala  
 100 105 110  
 Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly  
 115 120 125  
 Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly  
 130 135 140  
 Ile Tyr Ser Gln Ile Ala Val Thr Cys Thr Gln Gly Ser Ala Asn  
 145 150 155 160  
 Cys Ile Thr Ala Gln Asp Leu Gln Val Ala Ser Thr Val Ser Pro  
 165 170 175  
 Ala Gln Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Gln Ala Arg  
 180 185 190  
 Gly Thr Asp Pro Lys Arg Leu Gln Gly Leu Ile Met Pro Gly Gln Tyr  
 195 200 205

1123 1171 1219 1266

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile 210  
 Thr Arg Ser Ala Asn His Phe Gln Gln Thr Asp Ile Thr Gly Arg Ala 225  
 Asp Ala Ile Gly Leu Thr Pro Tyr Gln Leu Val Thr Ala Ala Ser Leu 245  
 Ile Gln Arg Gln Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val 260  
 Ile Leu Asn Arg Leu Ala Gln Pro Met Gln Leu Gln Phe Asp Ser Thr 275  
 Val Asn Tyr Gly Leu Ser Gln Gln Val Ala Thr Thr Asp Gln Asp 290  
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro 305  
 Gln Thr Pro Ile Ala Val Ser Thr Gln Ala Leu Gln Ala Met Gln 325  
 Asn Pro Ala Gln Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp 340  
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 Met Ile Gly Ala Ile 1  
 5  
 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro 20  
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Gln Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly 35  
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259

307	ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc	Pro Leu Pro	55	gag cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc	Pro Leu Pro	40	Gln Pro Val
355	gac tgg tcc gcc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc	Asp Trp Ser	70	gac tgg tcc gcc ggc ggc aca gtc gtc acc gaa atc cct aaa agc ggc	Asp Trp Ser	75	Val Val Val
403	tgg atc atg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	Trp Ile Met	90	tgg atc atg ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc	Trp Ile Met	95	Val Val Val
451	gac gtc tta gaa ata acg ctt atc gac gcc acc ttc gat gtc tcc act	Asp Val Leu	105	gac gtc tta gaa ata acg ctt atc gac gcc acc ttc gat gtc tcc act	Asp Val Leu	110	Val Val Ser
499	ccc gtc tac gca ccc gaa atc ccg ggc aac ttc aac ttc gat gac gaa	Pro Val Tyr	120	ccc gtc tac gca ccc gaa atc ccg ggc aac ttc aac ttc gat gac gaa	Pro Val Tyr	130	Val Val Ser
547	tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac	Ser Gln Trp	135	tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac	Ser Gln Trp	145	Val Val Ser
579	atc aag gtt taaggagcaa acaacatgag caa	Ile Lys Val	150	atc aag gtt taaggagcaa acaacatgag caa	Ile Lys Val		
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<211> 152							
<212> PRT							
<213> Corynebacterium glutamicum							
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20	Gly Thr Asp Met Pro Trp His Ile Pro Gln Asp Leu Lys His Phe Lys		25	Gly Thr Asp Met Pro Trp His Ile Pro Gln Asp Leu Lys His Phe Lys		30	
35	Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln		40	Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Gln		45	
50	Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser		55	Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Gln Asn Phe Ile Leu Ser		60	
65	Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln		70	Ser Arg Gln Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Gln		75	
80			85			90	
	Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Gln Val Tyr Lys Ala		95	Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Gln Val Tyr Lys Ala		100	
	Thr Val Gly Ser Ala Asp Val Leu Ile Thr Leu Ile Asp Ala Thr		105	Thr Val Gly Ser Ala Asp Val Leu Ile Thr Leu Ile Asp Ala Thr		110	
	100		115			120	
	Thr Val Gly Ser Ala Asp Val Leu Ile Thr Leu Ile Asp Ala Thr		125	Thr Val Gly Ser Ala Asp Val Leu Ile Thr Leu Ile Asp Ala Thr		130	
	110		125			130	
	Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe		125	Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe		130	
	115		125			130	
	Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe		125	Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Gln Ile Pro Ala Asn Phe		130	

[illegible]

[illegible]

390	Asp Trp Gln Lys Cys Val	395	Ile Ala Lys Gln Thr Arg Asp Gly	400		405	
1363	gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc	410	Ala His Met Leu Asp Leu Cys Val Tyr Val Gly Thr	415		420	
1411	gca gat atg gca acc tga gca gca ctt ctt gct acc acc gtc act ttg	425	Ala Asp Met Ala Thr Leu Ala Leu Ala Thr Ser Ser Thr Leu	430		435	
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1507	gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttg gaa gac	455	Gln His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Gln Asp	460		465	
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1651	gca cgt acc gct gag cac aag gtt gca gca gca gca gca gca gca gca	505	Ala Arg Thr Ala Gln His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	510		515	
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1795	ggc atc gaa acc atc gaa gca gca gca gca gca gca gca gca gca gca	550	Gly Ile Gln Thr Ile Gln Ala Ile Arg Gln Leu Lys Lys Leu Tyr Pro	555		560	
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1939	gag gct ggt ggt ctg gac tct gca att gca cag cag cag cag cag cag	595	Gln Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	600		605	
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Val Leu Arg	65	Gln Ile His Arg	70	Ala Tyr Phe	75	Gln Ala Gly Asp Leu	80
Val Gln Thr	85	Asn Thr Phe	85	Gly Cys Asn Leu	90	Pro Asn Leu Ala Asp	95
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Ala Arg Gln	115	Val Ala Asp	120	Gln Met Gly Pro	125	Gly Met Arg	
Arg Phe Val	130	Val Gly Ser	135	Leu Gly Thr	140	Lys Leu Pro Ser Leu	
Gly His Ala	145	Pro Tyr Ala	150	Asp Leu Arg	155	Gly His Tyr Lys Gln Ala	160
Leu Gly Ile	165	Ile Asp Gly Gly	170	Ala Phe Leu	175	Ile Gln Thr Ala	
Gln Asp Leu	180	Gln Val Lys	185	Ala Val His	190	Gly Val Gln Asp Ala	
Met Ala Gln	195	Leu Asp Thr	200	Phe Leu Pro	205	Ile Cys His Val Thr Val	
Gln Thr Thr	210	Thr Gly Thr	215	Met Leu Met	220	Gly Ile Gln Ala Ala Leu	
Thr Ala Leu	225	Gln Pro Leu	230	Gly Ile Asp Met	235	Ile Gly Leu Asn Cys Ala	240
Thr Gly Pro	245	Asp Gln Met	250	Ser Gln His	255	Leu Ser Lys His	
Ala Asp Ile	260	Pro Val Ser	265	Val Met Pro	270	Asn Ala Gly Leu Pro Val Leu	
Gly Lys Asn	275	Gly Ala Gln	280	Tyr Pro Leu	285	Ala Asp Leu Ala Gln	
Ala Leu Ala	290	Gly Phe Val	295	Ser Gln Tyr	300	Gly Leu Ser Met Val Gly Gly	
Cys Cys Gly	305	Thr Thr Pro	310	Gln His Ile	315	Arg Ala Val Arg Asp Ala Val	320
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 Val Ala Tyr Leu Gln Pro Phe Met Gln Gln Ala Gln Ala Thr Gly 740  
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 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser 770  
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 Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 785  
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 1 Met Ser Thr Ser Val  
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 10 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Gln Phe Leu Asp Ala  
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 25 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
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355	Ala Ser	Leu Tyr	Thr Ser	Val Pro	Leu Ser	Gln Thr	Gly Ile	Ser	390
370	Met Ile	Gly Gln	Arg Thr	Asn Ser	Asn Gly	Ser Lys	Ala Phe	Arg Gln	405
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415	Gln Thr	Arg Asp	Gly Ala	His Met	Leu Asp	Leu Cys	Val Asp	Tyr Val	450
420	Gly Arg	Asp Gly	Thr Ala	Asp Met	Ala Thr	Leu Ala	Ala Leu	Ala	465
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495	Met Lys	Leu Val	Lys Gln	His Gly	Ala Val	Ala Leu	Val Thr	Ile	540
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515	Lys Arg	Leu Ile	Asp Asp	Ile Thr	Gly Ser	Tyr Gly	Leu Asp	Ile Lys	570
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1219	ggc ggc aac atc gac gcg gct gct gtc gat gcg gcg tcc gca gca att	Ala Gly Asn Ile Asp Ala Phe Asp Ala Ala Ser Ala Ala Ile	360
1267	gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Gln Leu	375
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1363	aag tca ctg gag ctt cca gct ctg cca acc acc acc acc att ggt tct ttc	Lys Ser Leu Gln Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	410
1411	cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Gln	425
1459	tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat		435

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	550															
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	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln	Trp	Ser	Val	Asp	Ser	Phe	Arg
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	Ala	Asp	Val	Thr	Thr	Ile	Glu	Ala	Ala	Arg	Ser	Asp	Met	Gln	Val	Leu
	650															
2131	gct	gct	ctg	aaa	tct	tcc	ggc	ttc	gag</							

680	695	Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val	705	2227
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	745	Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile		2358
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	45		55	
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	70		85	
	85	Pro Glu Arg Phe Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro	90	
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	110		125	
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	130	Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala	155	
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	150		170	
	165	Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr	175	
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340											
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Phe	Ser	Gln	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	505
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Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Gln Pro Ala Ile Arg Glu  
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625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Ile Gln Ala Ala Arg Ser  
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660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala  
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Gln Lys Val Asp Gly Leu Leu Gln Ala Ala Leu Gln Ser Val Asp Pro  
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Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp  
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Met Thr Ser Asn Phe  
1  
5



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259	ctt gcg cag acc gcc cgc caa tgg gtc aac act gca tgg gat tct tgg	Leu Ala Gln Thr Ala Arg Gln Val Asn Thr Ala Ser Asp Ser Leu	50
307	tct gga tgg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	65
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403	gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	95
451	tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	110
499	acc aag tgg ttt gat acc aac tac cac tac ctc gtc ccg gag tgg tct	Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	125
547	gcg gat aca cgt ttc gtt tgg gat ggc tcc gcg cgt att gag gat ctc	Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	145
595	cgt tgc cag cag gtt cgt ggc ggt aat ggc cgc cct gtt ctg gtt ggt	Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	160
643	cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Asp Gly Ser Asn Pro	175
691	tgg gat cac cag cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	190
739	tct ttc gat act gag tgg gtt cag atc gat gag cct gcg tgg gtc acc	Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	210
787	gat gtt gct cct gag gtt tgg gag cag gtc cgc gct ggt tac acc act	Asp Val Ala Pro Glu Val Leu Gln Val Arg Ala Gly Tyr Thr Thr	225
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			245

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 1651 Arg Cys Val Arg Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515  
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 50 55 60  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 65 70 75 80  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 85 90 95  
 Pro Gln Arg Phe Asp Asp Ile Ala Asp His Gln Asn Asp Gly Leu Pro  
 100 105 110  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Gln Thr Leu  
 115 120 125  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu

123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala	130	135	140
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Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr	180	185	190
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu	195	200	205
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Val Arg	210	215	220
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr	225	230	235
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Val Ala Gly Ile Val Asp Gly	275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val	325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu	340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Phe Asp Ala	355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385	390	395
Val Thr Leu Glu Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala	420	425	430
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Ala Met	435	440	445

Arg Gln Ile Asp Leu Val Ile Ala Lys Gln Gln Leu Gly Leu 450 455 460

Asp Val Leu Val His Gly Gln Pro Gln Arg Asn Asp Met Val Gln Tyr 465 470 475 480

Phe Ser Gln Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val 485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn 500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln 515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr 530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr 545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Gln Ile Asn Asp Leu Ile 565 570 575

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Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln 10 15 20

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Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp 25 30 35

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Val Gln Ile His Thr His Met Cys Tyr Ser Gln Phe Asn Gln Val Ile 40 45 50

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Thr Ile Gln Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys 65  
Ser Ser Gly Phe Gln Leu Gly Val Gly Pro Gly Val Trp Asp Ile His 85  
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 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Gln Leu 20  
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 ttc cag att ctg cag tct tct gta gat gag gtc atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val 50  
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 Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Gln Tyr Gly His Val Thr 65  
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 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu 50  
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 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr 180  
 Asn Lys Phe Tyr Asp Thr Asp Glu Val Val Ala Cys Ala Asp 195  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val 210  
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96	agc gtg aag gat	tac tyr	ltg leu	asp trp	ile ile	gtg arg	thr arg	cgc atc	gat gat	ala ala	ile	30
144	aac agt gca	gtg val	lys gln	gag gln	gaa gln	cag acc	cgc arg	ctg cac	atc ile	asn ser	ala	35
192	tcg tgg	gln asp	thr asp	act gac	gag atc	gln thr	arg leu	his ile	glt gln	glt gln	val	60
240	gac atc	atc ile	asp ile	gag gln	gca ala	gag gln	gag val	glt gln	glt gln	glt gln	phe	80

[illegible]

Cys Gly Leu Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu 145  
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 Gln Ser Leu Val Gln Gly Ala Arg Ile Ala Ser Lys Gln Leu Phe 165  
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 Met Ser Gln Asn Arg 1  
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atc agg acc acc cag gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Gln Leu 20  
 15

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Gln Ile Gly Gln Gln Phe 35  
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ttc cag att ctc cag tct tct gta gat gag gtc atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Val Ile Lys Arg Gln Val 50  
 45

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Gln Tyr Gly His Val Thr 65  
 60

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg 85  
 80

ctg ggc gga ctc acc atg acc gat acc gag cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Gln 100  
 95

gca gtc cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Gln Leu Thr Ser Phe Ser Asp 115  
 110

cgt cgc gac cgc gca ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Gln Ala Tyr Gln Asp Pro Val Ser 130  
 125

ggc atc ttc acc ggt cgc gct tct gtc ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Gln Phe Thr Gly 145  
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cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595

Pro Ile Thr Tyr Ile Gly Gln Gln Thr Gln Thr Asp Val Asp Leu	150	155	160	165
643	ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtc gca	170	175	180
691	gca cta tcc cca gga tct gca gct cga ttc acc aac aag ttc tac gac	185	190	195
739	act gat gaa gaa gaa gtc gtc gca gca tgc gct gct gac ggc ctc cag gaa	200	205	210
784	tac aag atc atc acc gat gca gct ctg acc gtc cag ctc gac gca	215	220	225
	Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala			
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	Thr Pro Gln Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Gln Ile	20	25	30
	Gly Gln Gln Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Val	35	40	45
	Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Gln Gly Gln	50	55	60
	Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn	65	70	75
	Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg	85	90	95
	Trp Ala Ser Gln Gln Ala Val Arg Ser Thr Pro Gly Asn Ile Gln Leu	100	105	110
	Thr Ser Phe Ser Asp Arg Asp Arg Ala Leu Phe Ser Gln Ala Tyr	115	120	125
	Gln Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn	130	135	140
	Pro Gln Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Gln Thr Gln	145	150	155
	Thr Asp Val Asp Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr	165	170	175
	Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr	180	185	190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Cys Ala Asp 195  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val 210  
 Gln Leu Asp Ala 225

&lt;210&gt; 725

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (1)..(528)

&lt;223&gt; RXS02197

&lt;400&gt; 725

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 Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe 1  
 ttc tgc atc gcg gat ttc atc cgc cca cgc gag caa gct gtc aag gac 20  
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp 25  
 ggc caa gtc gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 30  
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro 45  
 att gct gat ttc gcc aac gag ttc gca gcc aat gaa tac cgc gag 60  
 Ile Ala Asp Phe Ala Asn Glu Tyr Arg Glu 75  
 tac ttc gaa gtt cac ggc atc ggc gtc cag ctg acc gaa gca ttc ggc 80  
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala 90  
 gag tac tgc cac tcc cga gtc cgc agc gaa ctc aag ctg aac gac ggt 95  
 Gln Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly 110  
 gga tct gtc gct gat ttc gat cca gaa gac aag acc aag ttc ttc gac 125  
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Asp 140  
 ctc gat tac cgc ggc ggc ggc ttc ttc ttc ggt ttc ggt tac ggt tct tgc cct 155  
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro 160  
 gat ctc gaa gac gac cgc gca aag ctg gaa ttc gtc gac cca gag cag tcc 175  
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg 190  
 atc ggc gtc gag ttc tcc gag gaa ctc cag ctg cac cca gag cag tcc 205  
 Ile Gly Val Glu Ser Glu Ser Glu Ser Glu Leu His Pro Glu Gln Ser 220  
 145

aca gac gcg ttg gtc ctc tac cac cca gag gca aag tac ttt aac gtc  
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

551

taacaccctt gagaggggaaa act

&lt;210&gt; 726

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 726

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Arg Gly Arg Phe  
 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp  
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro  
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu  
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala  
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly  
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp  
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro  
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Glu Pro Gly Arg  
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Glu His Pro Glu Gln Ser  
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val  
 165 170 175

&lt;210&gt; 727

&lt;211&gt; 546

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(523)

&lt;223&gt; RXC00988

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Met Ser Lys Arg Gln 1  
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gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag  
Gln Ser Ile Gln Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys 20  
163

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gta atg  
Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met 35  
211

gaa gca atc acc tta ggt ctt gtc ctc acc gtc atc ctg cgc gtc gac  
Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp 50  
259

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc  
Asp Gly Ile Tyr Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val 65  
307

gcg atc gca cac ttc gtt gct gca ttc ctg caa agt ttc agt tgg tcc  
Ala Ile Ala His Phe Val Ala Phe Leu Gln Arg Phe Ser Trp Ser 85  
355

atc ccg atg aac atc gtc ctg cag gtt ctt gca ctt gca ctt ggt ttc  
Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe 100  
403

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc ggc tgg  
Val His Pro Ala Met Gly Phe Ala Ile Ile Phe Ile Ala Trp 115  
451

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc  
Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg 130  
499

ggg ctg ctt acc acg cag cac agc taagcttaa ggcctccgg ggc  
Gly Leu Leu Thr Thr Gln His Ser 140  
546

<210> 728

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<212> PRT

<213> Corynebacterium glutamicum

<400> 728

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His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala 20  
25 30

Gly Thr Leu Val Met Gln Ala Ile Thr Leu Gly Leu Val Thr Val 35  
40 45

Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val 50  
55 60



Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln 65  
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala 85  
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile 100  
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile 115  
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser 130  
 135  
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<220>  
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 Val Ala Phe Met Gln 1  
 aaa acg tca cgc ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163  
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala 20  
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211  
 Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile 35  
 tcc atc acg gta tcc atc act ttt tgg ttg tgg ggc gtt gtt tgt ggt 259  
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly 50  
 ttc gca ggt ttg aag gtc caa ggt cgc ctc gat gag ggg gtt atc ggc 307  
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Gln Gly Leu Ile Gly 65  
 cag gac aaa tcc caa atg aac ccc gtt acc att gcc tat ctt ggc atg 355  
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met 85  
 ctg ggt cga cgc ggt tgg ggt ggc gga att ttc ggc ggc ggt tat 403  
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr 100  
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451  
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Gln Leu Ser Ala 115

gca tcg aat gat ctt ccg gga ggt att gcc tgt gcg ctg gga atc 499  
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile  
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547  
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Gln Arg Ser Cys Gln Ala Pro  
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatggaatc 594  
 Pro Pro Gln Ser Gly Gln Ala Ile Ser  
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 aag 597

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Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp

Gln Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala

Gly Gln Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Gln Arg

Ser Cys Gln Ala Pro Pro Gln Ser Gly Gln Ala Ile Ser

<213> Corynebacterium glutamicum

<212> DNA

<211> 723

<210> 731

<220>

<221> CDS

<222> (101) .. (700)

&lt;223&gt; RXC01942

&lt;400&gt; 731

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gtgatcaagg tcaacggcaa gaacgagtaa cctgggatcc atg ttg cgc att gga 115

Met Leu Arg Ile Gly  
1

5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt ggc gat ctt ttg 163

Leu Thr Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt ggc cgc gat 211

Ser Ser Gln Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gac gaa gct ttt 259

Ile Val Gln Pro Gly Gln Pro Ala Leu Ala Gln Leu Ala Gln Phe 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac gcg gga tta 307

Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctc aat gcc 355

Ala Ala Lys Ala Phe Val Ser Gln Gln Thr Ala Leu Leu Asn Ala 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403

Ile Thr His Pro Arg Ile Ala Gln Ser Ala Arg Arg Phe Asn Gln 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451

Ala Gln Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gta gtt gat 499

Val Gln Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Asp 130

glt gac gta gag gaa cgc gtc cgc aga ctt gtc gaa aaa cgt ggc ctc 547

Val Asp Val Gln Arg Val Arg Arg Leu Val Gln Lys Arg Gly Leu 145

aca gag gac gac gtc cgc cgt cga atc gct tct caa gtc ccc gac gac 595

Thr Gln Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp 165

gtc aga ctt aaa gcc gtc gac atc gtc gtc gac aat aac ggc acg cta 643

Val Arg Leu Lys Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu 180

gag gac ctt cat gct gaa gca agc aag ctc att gct gag att ctt agt 691

Gln Asp Leu His Ala Gln Ala Ser Lys Leu Ile Ala Gln Ile Leu Ser 195

cgc gtc aat tagcactaaa acatcgctcaa agt 723

Arg Val Asn 200

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Ala Glu Ile Leu Ser Arg Val Asn

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163	atc ggc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa	Ile Ala Arg	10	atc ggc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa	Ile Ala Arg	20	1	Val Lys Asn Leu Asp	5
211	aaa caa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc	Lys Gln Gln	25	aaa caa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc	Lys Gln Gln	35	21		
259	ggc ctc ggc tca ccc gcc ctc ctc tac ctt gct ggc gct ggc ggc ggc	Gly Leu Gly	40	ggc ctc ggc tca ccc gcc ctc ctc tac ctt gct ggc gct ggc ggc ggc	Gly Leu Gly	50	259		
307	cac atc cac atc atc atc gac gat gac ctc gtc gac ctc tcc aac ctc cac	His Ile His	55	cac atc cac atc atc atc gac gat gac ctc gtc gac ctc tcc aac ctc cac	His Ile His	65	307		
355	cgc cag gtc atc cac acc acc gct ggc ggt gga aca ccc aag gcc gag	Arg Gln Val	70	cgc cag gtc atc cac acc acc gct ggc ggt gga aca ccc aag gcc gag	Arg Gln Val	80	355		
403	tcc gcg cgc gaa gca atg ctc gca ctc gac ctc aac cct tcc gtc aaa gtc acg	Ser Ala Arg	90	tcc gcg cgc gaa gca atg ctc gca ctc gac ctc aac cct tcc gtc aaa gtc acg	Ser Ala Arg	95	403		
451	ggt tct gtc agg cga ctc gac tgg tca aat gca ctt tct gag ctc gca	Val Ser Val	105	ggt tct gtc agg cga ctc gac tgg tca aat gca ctt tct gag ctc gca	Val Ser Val	115	451		
499	gat tcc gat gtc atc tgc gat ggc tcc gat aac ttc gac acc cga cac	Asp Ser Asp	120	gat tcc gat gtc atc tgc gat ggc tcc gat aac ttc gac acc cga cac	Asp Ser Asp	130	499		
547	ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca	Leu Ala Ser	135	ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca	Leu Ala Ser	145	547		
595	tcc atc ctc ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac	Ser Ile Leu	155	tcc atc ctc ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac	Ser Ile Leu	160	595		
643	ggc ccc atc tac gaa gac ctc ttc ccc acc ccc gcc cca cca ccc gga tcc	Gly Pro Ile	170	ggc ccc atc tac gaa gac ctc ttc ccc acc ccc gcc cca cca ccc gga tcc	Gly Pro Ile	175	643		
691	gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta	Val Pro Ser	185	gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta	Val Pro Ser	190	691		
739	atg ggc tcc gcg atg gcc atg gaa gcc ctc gaa ggc ctc gaa ggc gtc	Met Gly Ser	200	atg ggc tcc gcg atg gcc atg gaa gcc ctc gaa ggc ctc gaa ggc gtc	Met Gly Ser	210	739		
787	ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc	Gly Thr Pro	215	ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc	Gly Thr Pro	225	787		
835	acc tgg gaa tac atc ccc gtc gtc ggt tcc ggc ggc ggc ggc ggc ggc	Thr Trp Gln	220	acc tgg gaa tac atc ccc gtc gtc ggt tcc ggc ggc ggc ggc ggc ggc	Thr Trp Gln	225	835		

230	235	240	245
gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag	Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Phe Gly Gln	883	931
Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu	265	270	275
atc gac gtc cgc gaa ccc tcc gaa ttc tcc ggc tac tcc atc ccc ggc	Ile Asp Val Arg Gln Pro Ser Gln Phe Ser Ala Tyr Ser Ile Pro Gly	979	1027
gcg cac aac acc cca ctg tcc ggc atc cgc gaa ggc gcc atc cca ccc	Ala His Asn Thr Pro Leu Ser Ala Ile Arg Gln Gly Ala Ile Pro Pro	1075	1123
tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc	Ser Val Ser Ala Gly Lys Gln Val Ile Val Tyr Cys Ala Ala Gly Val	1171	1194
atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg	Met Ser Ser Leu Asp Gly Ile Gln Gly Trp Leu Asp Ser Leu Gly		
taaaccaag gcgtgtgcc acc			
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<211> 357			
<212> PRT			
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<400> 734			
Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly	1	5	10
Gln Ile Gly Gln Gln Lys Gln Ser Leu Phe Asp Ala Lys Val Ser	20	25	30
Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Tyr Leu Ala	35	40	45
Gly Ala Gly Val Gly His Ile His Ile Asp Asp Leu Val Asp	50	55	60
Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly	65	70	75
Thr Pro Lys Ala Gln Ser Ala Arg Gln Ala Met Leu Ala Leu Asn Pro	85	90	95
Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala	100	105	110
Leu Ser Gln Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn			

115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Lys Leu Gly Ile  
 130 135 140  
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val  
 145 150 155  
 Phe His Ala Gly His Gly Pro Ile Tyr Gln Asp Leu Phe Pro Thr Pro  
 165 170 175  
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 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Gln Ala Leu Lys  
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 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr  
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 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Gln  
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Protein	Position	Sequence	Mass
Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg	65		80
Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Gln Val Leu Asp Val	50		60
Ile Pro Val Val Gly Ser Pro Gln Val Leu Gln Arg Val Leu Gly Ser	35		45
Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Gln Tyr	20		30
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Gln Ala Ile Ala Ile Leu Gln Ser Ala Gly Tyr Thr Gly Met Ser Ser	130		140
c a a g c c a t c g a a t t a g a a t c c g a g g a t a c c g a a t g a t g a c a g c			435
Ala Gly Lys Gln Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala	115		125
g c a g g t a a a g a g g t a t c g t c t a c t g c g c a g a t t c c g c a			387
Thr Pro Leu Ser Ala Ile Arg Gln Gly Ala Ile Pro Pro Ser Val Ser	100		110
a c c c c a c t g t c c g c c a t c c g c g a a g g c a t c c c a c c c c c t c c			339
Arg Gln Pro Ser Gln Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn	85		95
c g c g a a c c c t c c g a a t t c t c c g c c t a c t c c a t c c c g g c g c g c a c a a c			291
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val	65		75
g t t c c t c g a g t t c c g c g c t g t g a c g g c g t t c g c t c a t c g a c g t c			243
Ser Ala Gly Val Ser Gly Ile Ser Gly Ile Ser Gly Phe Gly Gln Val Leu Asp	50		60
t c t g c t g t g t t c g g g a t t c t g g c g g t t t g g t g a g g t g c t c g a t			195
Tyr Ile Pro Val Val Gly Ser Pro Gln Val Leu Gln Arg Val Leu Gly	35		45
t a c a t c c c c g t c g t c g g t c c g g a g g t g t c t g g a a c g g g t g c t g g g			147
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Gln	20		30
t t g a t c g a a a a c t c g g c t a c t a c t c c c t c c g a c g g c a c c t g g g a a			99